

SEQUENCE LISTING

<110> Genentech, Inc.
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<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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 35 40 45

Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
 50 55 60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
 65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
 85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
 100 105 110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
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Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
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Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
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Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
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Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
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Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
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Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
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Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
 260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
 275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys
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Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
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Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly			
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Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro			
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His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln			
130		135	140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
145	150	155	160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
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Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
180		185	190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His			
195		200	205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys			
210		215	220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn			
225	230	235	240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys			
245		250	255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln			
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Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys			
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Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu			
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His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His			
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<213> Artificial Sequence
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<212> PRT

<213> Homo sapiens

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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
35 40 45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
50 55 60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
 65 70 75 80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
85 90 95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
 100 105 110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
 115 120 125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
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His Asp Pro Gly

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					20			25				30			

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Pro	Ala	Ser	Tyr	Arg	Leu	Trp	Gly	Ala	Pro	Leu	Gln	Pro	Thr	Leu	Gly
	50				55				60						

Val	Val	Pro	Gln	Ala	Ser	Val	Pro	Leu	Leu	Thr	Asp	Leu	Ala	Gln	Trp
65					70				75			80			

Glu	Pro	Val	Leu	Val	Pro	Glu	Ala	His	Pro	Asn	Ala	Ser	Leu	Thr	Met
					85			90			95				

Tyr	Val	Cys	Thr	Pro	Val	Pro	His	Pro	Asp	Pro	Pro	Met	Ala	Leu	Ser
				100			105				110				

Arg	Thr	Pro	Thr	Arg	Gln	Ile	Ser	Ser	Asp	Thr	Asp	Pro	Pro	Ala	
				115			120			125					

Asp	Gly	Pro	Ser	Asn	Pro	Leu	Cys	Cys	Phe	His	Gly	Pro	Ala	Phe	
				130			135			140					

Ser	Thr	Leu	Asn	Pro	Val	Leu	Arg	His	Leu	Phe	Pro	Gln	Glu	Ala	Phe
145					150				155			160			

Pro	Ala	His	Pro	Ile	Tyr	Asp	Leu	Ser	Gln	Val	Trp	Ser	Val	Val	Ser
				165			170				175				

Pro	Ala	Pro	Ser	Arg	Gly	Gln	Ala	Leu	Arg	Arg	Ala	Gln			
				180			185								

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19

tgctgtgcta ctcctgc当地 gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

cccacgcgtc cgaacctctc cagcgatggg agccgcccgc ctgctgcccc acctcactct 60
 gtgttacag ctgtgttgc tctgtgtca aactcgtac gtgagggacc agggcgccat 120
 gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
 caagcacgtg caggtcacccg gggtcgcat ctccgccacc gccgaggacg gcaacaagt 240
 tgccaagctc atagtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300
 gagtgagaag tacatctgtt tgaacaagag gggcaagctc atcgggaagc ccagcggaa 360
 gagcaaagac tgcgtgttca cggagatcgt gctggagaac aactatacgg cttccagaa 420
 cggccggcac gagggtgtt tcattggccctt cacqcgccag gggcgcccc gccaggcttc 480
 cccagccgc cagaaccagc gcgaggccca cttcatcaag cgcctctacc aaggccagct 540
 gcccctcccc aaccacgccc agaagcagaa gcagttcgag tttgtggct ccgcggccac 600
 cccggccacc aagcgcacac ggccggccca gcccctcagc tagtctggga ggcaggggc 660
 agcagccctt gggccgcctc cccacccctt tcccttctta atccaaggac tgggtgggg 720
 tggcggagg ggagccagat ccccgaggga ggacccttag ggcgcgcaag catccgagcc 780
 cccagctggg aagggcagg ccgggtcccc agggcggtt ggcacagtgc ccccttccc 840
 gacgggtggc agggcccttga gaggaactga gtgtcacccct gatctcaggc caccagcctc 900
 tggccggccctc ccagccgggc tcctgaagcc cgctgaaagg tcagcgactg aaggccctgc 960
 agacaaccgt ctggagggtgg ctgtcctcaa aatctgttcc tcggatctcc ctcagtctgc 1020
 ccccgccccc caaactcctc ctggctagac tgttaggaagg gactttgtt tgggttttgc 1080
 ttccaggaaa aaagaaaaggg agagagagga aaatagaggg ttgtcoactc ctcacattcc 1140
 acgaccagg cctgcacccc acccccaact cccagccccg gaataaaacc atttcctgc 1200

<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23
 Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
 195 200 205

<210> 24
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 24
 cagtacgtga gggaccaggg cgccatga 28

<210> 25

aagggttt tgataatctc tccaacctga agcagctcac tgctcgaaat aacccttgg 1200
 tttgtgactg cagtattaaa tgggtcacag aatggctcaa atatatccct tcacatctca 1260
 acgtgcgggg tttcatgtgc caaggtccctg aacaagtccg ggggatggcc gtcagggaat 1320
 taaatatgaa tctttgtcc tgtcccacca cgacccccgg cctgcctctc ttcacccca 1380
 ccccaagtac agcttctccg accactcagc ctccccaccct ctctattcca aacccttagca 1440
 gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500
 gcagagaaaag agtgacccca cctatttctg aacggatcca gctctctatc cattttgtga 1560
 atgatacttc cattcaagtc agctggctct ctctcttac cgtatggca tacaaactca 1620
 catgggtgaa aatggccac agtttagtag ggggcacatcg tcaggagcgc atagtcagcg 1680
 gtgagaagca acacctgagc ctggtaact tagagccccg atccacctat cggatttgg 1740
 tagtgcact ggatgtttt aactaccgcg cggtagaaga caccatttgt ttagaggcca 1800
 ccacccatgc ctcttatctg aacaacggca gcaacacaggc gtccagccat gaggcagacga 1860
 cgtcccacag catggctcc ccctttctgc tggcgggctt gatcggggc gcggtgat 1920
 ttgtgctggt ggtcttgctc agcgtttttt gctggcatat gcacaaaaag gggcgctaca 1980
 cctccagaa gtggaaatac aaccggggcc ggcggaaaga tgattattgc gaggcaggca 2040
 ccaagaagga caactccatc ctggagatga cagaaaaccag tttcagatc gtctccttaa 2100
 ataacgatca actccttaaa ggagattca gactgcagcc catttacacc ccaaattggg 2160
 gcattaatta cacagactgc catatccccca aacaacatgcg atactgcaac agcagcgtgc 2220
 cagacctgga gcactgccat acgtgacagc cagaggccca gcggtatcaa ggcggacaat 2280
 tagactcttgc agaacacact cgtgttgca cataaaagaca cgcagattac atttgataaa 2340
 tgttacacag atgcatttgcgat actctgtat ttatacggtg tactatataa 2400
 tgggatttaa aaaaagtgc atctttcta tttcaagtttta attacaaca gttttgttaac 2460
 tctttgctt ttaaatctt 2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met	Gly	Leu	Gln	Thr	Thr	Lys	Trp	Pro	Ser	His	Gly	Ala	Phe	Phe	Leu
1															15

Lys	Ser	Trp	Leu	Ile	Ile	Ser	Leu	Gly	Leu	Tyr	Ser	Gln	Val	Ser	Lys
															30
20															

Leu	Leu	Ala	Cys	Pro	Ser	Val	Cys	Arg	Cys	Asp	Arg	Asn	Phe	Val	Tyr
															45
35															

Cys	Asn	Glu	Arg	Ser	Leu	Thr	Ser	Val	Pro	Leu	Gly	Ile	Pro	Glu	Gly
															60
50															

Val	Thr	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Ile	Asn	Asn	Ala	Gly	Phe
															80
65															

Pro	Ala	Glu	Leu	His	Asn	Val	Gln	Ser	Val	His	Thr	Val	Tyr	Leu	Tyr
															95
85															

Gly	Asn	Gln	Leu	Asp	Glu	Phe	Pro	Met	Asn	Leu	Pro	Lys	Asn	Val	Arg
															110
100															

Val	Leu	His	Leu	Gln	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Ser	Arg	Ala	Ala
															125
115															

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140

Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160

Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175

Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190

Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205

Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220

Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255

Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270

Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285

Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300

Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320

Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335

Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350

Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
 355 360 365

Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380

Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400

Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405 410 415

Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val
 420 425 430

Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met
 435 440 445

Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly
 450 455 460

Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
 465 470 475 480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu
 485 490 495

Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala
 500 505 510

Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser
 515 520 525

His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala
 530 535 540

Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser
 545 550 555 560

Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys
 565 570 575

Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly
 580 585 590

Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln
 595 600 605

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu
 610 615 620

Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His
 625 630 635 640

Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu
 645 650 655

His Cys His Thr
 660

<210> 29
<211> 21
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29

cgggtctacct gtagtggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30

gcaggacaac cagataaaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32

ttcacgggct gctttgcc agctttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttggagca agcggcgccg gcggagacag aggcagaggc agaagctggg gctccgtcct 60
cgctcccac gagcgatccc cgaggagac cgccggccctc ggcgaggcga agaggccgac 120

gaggaagacc cgggtggctg cgccctgcc tcgcttcca ggcccggcg gtcgcggct 180
 tgccccttt gctcgccctg aaaatgaaa agatgctcgc aggctgctt ctgcgtatcc 240
 tcggacagat cgtcttcctc cctgcccagg ccagggagcg gtcacgtggg aggtccatct 300
 ctagggccag acacgctcg acccaccgcg agacggccct tctggagagt tcctgtgaga 360
 acaaggccccg agacctggtt ttcatcattg acagctctcg cagtgtcaac accccatgact 420
 atgcaaaggta caaggagttc atcgtggaca tcttgcattt cttggacatt ggtcctgatg 480
 tcaccccgagt gggcctgctc caaatatggca gcactgtcaa gaatgagttc tccctcaaga 540
 ccttcaagag gaagtcccgag gtggagcggtg ctgtcaagag gatgcggcat ctgtccacgg 600
 gcaccatgac tgggtggcc atccagatg ccttgcacat cgcattctca gaagcagagg 660
 gggcccgcc cctgaggggag aatgtccac ggttgcataat gatcgtgaca gatggggagac 720
 ctcaggactc cgtggcccgag gtggctgcta aggcacggga cacgggcattc ctaatcttg 780
 ccattggtgtt gggccaggta gacttcaaca ctttgcagtc cattggaggt gagccccatg 840
 aggaccatgt ctcccttgcg gccaatttca gccagattga gacgctgacc tccgtgttcc 900
 agaagaaggta gtgcacggcc cacatgtgca gcaccctggaa gcataactgt gcccacttct 960
 gcatcaacat ccctggctca tacgtctgca ggttgcacatc aggctacatt ctcaactcg 1020
 atcagacgac ttgcagaatc caggatctgt gtggccatggaa ggaccacaaac tgtgagcagc 1080
 tctgtgtgaa tggccggcc tccttcgtct gccagtgctc cagtggctac gcccctggctg 1140
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 agcatgatgt cgtaacatg gaggagagct actactgcgc ctgcaccgt ggctacactc 1380
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 cagccaaaga catgaaaaaaa gccgtggccc acatgaaata catggaaaag ggctctatga 2280
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 gatacagatg aagatttagaa atcgcgacac attgttagtc attgtatcac ggattacaat 3000
 gaacgcagtg cagagccccca aagctcaggc tattgtttaaa tcaataatgt tttgtgttggaa 3060
 aacaatcagt actgagaaaac ctgggttgc acagaacaaa gacaagaagt atacactaac 3120
 ttgttataat ttatcttagga aaaaaatcct tcagaattct aagatgttattt taccaggta 3180
 gaatgaataa gctatgcagtg gatattttgttataactgtg gacacaactt gcttctgcct 3240
 catcctgcct tagtgcgttcaatcatttgcata aagtttgcac agtcttactt 3300

ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggacttac cttgatata 3360
 gtatatggat gtatgcataa aatcatagga catatgtact tgtggAACAA gttggatttt 3420
 ttatacaata ttaaaaattca ccacttcag 3449

<210> 34
 <211> 915
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
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 Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
 20 25 30
 Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
 35 40 45
 Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
 50 55 60
 Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
 65 70 75 80
 Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
 85 90 95
 Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
 100 105 110
 Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
 115 120 125
 His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
 130 135 140
 Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
 145 150 155 160
 Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
 165 170 175
 Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
 180 185 190
 Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
 195 200 205
 Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
 210 215 220
 Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245	250	255	
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260	265	270	
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275	280	285	
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290	295	300	
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325	330	335	
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340	345	350	
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355	360	365	
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370	375	380	
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405	410	415	
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420	425	430	
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435	440	445	
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450	455	460	
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485	490	495	
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500	505	510	

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
 Val Gly Lys Ala Ile Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910

Arg Tyr Arg
 915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 36

acagccatgg tctatacgctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37
gcctgtcaagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38
<211> 1813
<212> DNA
<213> Homo sapiens

<400> 38
ggagccgccc tgggtgtcag cggctcggt cccgcgcacg ctccggccgt cgccgcaggct 60
ccgcacactgc aggtccgtgc gtccccggc tggcccccgt gactccgtcc cggccaggga 120
ggccatgtat ttccctcccg gggcccttgg tgaccaactt gctgggggtt ttgttccctgg 180
ggctgagtgc cctcgccccc ccctcgccgg cccagctgca actgcacttg cccgcacaacc 240
ggttgcaggc ggtggaggga ggggaagtgg tgcttccagc gtggtaacacc ttgcacgggg 300
aggtgttttc atcccagcca tgggaggtgc ctttgtat gtggtttttc aaacagaaaag 360
aaaaggagga tcaggtgttg tcctacatca atggggtaac aacaagcaaa cctggaggat 420
ccttggtcta ctccatgccc tcccgaaacc tgccctgcg gctggagggt ctccaggaga 480
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atggggagga gcctccaccc accccctgact cctccttatg aagccagctg ctgaaattag 1560
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taaaaactaac atgaaatatg tgggttttc atttgcataat taaaataaag atacataatg 1800
tttgtatgaa aaa 1813

<210> 39
<211> 390
<212> PRT
<213> Homo sapiens

<400> 39
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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Phe Leu Gly Leu Ser Ala		Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln	
20		25	30
Leu His Leu Pro Ala Asn Arg		Leu Gln Ala Val Glu Gly Gly Glu Val	
35		40	45
Val Leu Pro Ala Trp Tyr Thr		Leu His Gly Glu Val Ser Ser Ser Gln	
50		55	60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85		90	95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100		105	110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115		120	125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130		135	140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145		150	155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165		170	175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180		185	190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195		200	205
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210		215	220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225		230	235
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245		250	255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260		265	270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275		280	285

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
 355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
 370 375 380

Gln Ala Gly Ser Leu Val
 385 390

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 40

agggtctcca ggagaaaagac tc

22

<210> 41

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 41

attgtgggcc ttgcagacat agac

24

<210> 42

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 42		
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc		50
<210> 43		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 43		
gtgtgacaca gcgtgggc		18
<210> 44		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 44		
gaccggcagg cttctgcg		18
<210> 45		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 45		
cagcagcttc agccaccagg agtgg		25
<210> 46		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 46		
ctgagccgtg ggctgcagtc tcgc		24
<210> 47		

<211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 47
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

 <210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

 <400> 48
 cgccaccact gcggccaccg ccaatgaaac gcctcccgct cctagtggtt tttccactt 60
 tggtaattt ttcctatact caaaaatttgc ccaagacacc ttgtctccca aatgcggaaat 120
 gtgaaatatacg caatggattt gaagcctgct attgcaacat gggattttca ggaaatgggt 180
 tcacaattttg tgaagatgtt aatgaatgtt gaaattttac tcagtcctgt ggcggaaaat 240
 ctaattgcac taacacagaa ggaagtttattt attgtatgtt tgtagcccttgc ttccatccca 300
 gcagtaacca agacagggtt atcactaatg atggaaccgtt ctgtatagaa aatgtgaatg 360
 ccaaactgcca ttttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaaa 420
 tcagatccat aaaagaacccgtt gtggcttgc tacaagaatg ctatagaaat tctgtgacag 480
 atctttcacc aacagatata attacatata tagaaatattt agctgaatca tcttcatttt 540
 tagttacaa gaacaacactt atctcagccca agacaccctt ttcttaactca actcttactg 600
 aatttgtaaa aaccgtgaaat aattttgttc aaagggtatc attttagttt tgggacaatg 660
 tatctgtgaa tcataggaga acacatcttta caaaactcat gcacactgtt gaacaagcta 720
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 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgtt tcatcatctg 960
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 cttcagtaat ttcaagtctca atgagctcaa acccaccac attatatgaa cttggaaaaaa 1080
 taacatttac attaagtcat cggaaagtca cagataggtt taggagtctt tttgcattttt 1140
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 agacttctgt ttgctaaatc tgtttcttt tctaataattc taaaaaaaaaaa aaaaaggTTT 2760
 acctccacaa attgaa 2820
 aa 2822

<210> 49
 <211> 690
 <212> PRT
 <213> Homo sapiens

<400> 49
 Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
 1 5 10 15
 Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
 20 25 30
 Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
 35 40 45
 Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
 50 55 60
 Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
 65 70 75 80
 Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Asn Gln
 85 90 95
 Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
 100 105 110
 Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
 115 120 125
 Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
 130 135 140
 Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
 145 150 155 160
 Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
 165 170 175
 Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685

Leu Arg
 690

<210> 50
 <211> 589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (61)

<223> a, t, c or g

<400> 50

tggaaacata tcctccctca tatgaatatg gatggagact acataaaatat atttccaaag 60
 ngaaaagccg gcatatggat tcaaattggca atgttcgcgt tgcatttta tattataaga 120
 gtattgtcc ct当地gcttgc atcatctgac aacttcttat tgaaacctca aaattatgtat 180
 aattctgaag aggaggaaag agtcataatct ttagtaattt cagtcataat gagctcaaac 240
 ccaccacat tatataact tgaaaaata acatttacat taagtcatcg aaaggcaca 300
 gataggtata ggagtctatg tggcatttg gaatactcac ctgataccat gaatggcagc 360
 tggcttcag agggctgtga gctgacatac tcaaattgaga cccacacccat atgccgctgt 420
 aatcactga cacatttgc aattttgatg tcctctggc cttccattgg tattaaagat 480
 tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgc 540
 atatgcattt ttacattctg gttcttcagt gaaattcaaa gcacccagg 589

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 52

ggagtagaaaa gcgcattgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54
cgagctcgaa ttaattcg 18

<210> 55
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55
ggatctcctg agtcagg 18

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56
cctagtgtgag tgatccttgt aag 23

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57
atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcatt 50

<210> 58
<211> 2137
<212> DNA
<213> Homo sapiens

<400> 58
gctcccagcc aagaacctcg gggccgctgc gcgggtgggg aaggttcccc gaaaccggc 60
cgctaagcga ggcctcctcc tcccgacat ccgaacggcc tgggcgggtt caccggct 120

gggacaagaa gccgcgcct gcctgcccgg gcccggggag ggggtgggg ctggggccgg 180
 aggcggttg tgagtgggtg tggcggggg gggaggctt gatcaatcc cgataagaaa 240
 tgctcggtg tcttggcac ctaccgtgg ggcccgttaag ggcgtactat ataaggctgc 300
 cggccggag ccgcgcgc gtcagacag gagcgtgcg tccaggatct agggccacga 360
 ccatcccaac cggcactca cagccccca ggcgcattcc gtcgcgcgc agcctccgc 420
 accccatcg cggagctgc gccgagagcc ccagggaggt gccatgcggc gcgggtgtgt 480
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 cagtgc当地 cagcggcagc tgtacaagaa cagaggctt cttccactct ctcatttcct 960
 gcccattctg cccatggtcc cagaggagcc tgaggacctc agggccact tggaaatctga 1020
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 ggaggccgtg aggagttccca gctttgagaa gtaactgaga ccatggccgg gcctttcac 1140
 tgctgc当地 ggctgtggta cctgcagcgt gggggacgtg cttctacaag aacagtctc 1200
 agtccacgtt ctgttagtct tttaggaagaa acatctagaa gttgtacata ttcagagtt 1260
 tccattggca gtgccagttt ctggccataa gacttgtctg atcataacat tgtaaggctg 1320
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 aaaattctta tgtcaagctg aaattctcta attttttctc atcacttccc caggagcagc 1500
 cagaagacag gcagtagttt taatttcagg aacagggtat ccactctgta aaacagcagg 1560
 taaatttcac tcaaccccat gtgggaaattt atcttatatct ctacttccag ggaccatttg 1620
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 ccatctccca gccaccaggc cctctgccc cctcacatgc ctcccatgg attggggcct 1860
 cccaggcccc ccaccttgc tcaaccttgc ctcttgc 35 40 45
 atttgaagac cccaagtctt gtcaataact tggctgtgg aagcagcggg ggaagaccta 1920
 gaacccttccca cccagactt ggtttccaa catgatattt atgagtaatt tattttgata 1980
 tgtacatctc ttatttctt acattattta tgcccccaaa ttatattt gatgttaagt 2040
 gaggttgggtt ttgtatatta aaatggagtt tggttgt 2100
 2137

<210> 59
<211> 216
<212> PRT
<213> Homo sapiens

<400> 59
Met Arg Ser Gly Cys Val Val Val His Val Val Trp Ile Leu Ala Gly Leu
1 5 10 15
Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
20 25 30
His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
35 40 45
Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 60
 atccgccccag atggctacaa tgtgtta 26

<210> 61
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 61
 gcctcccggt ctcccgtgagc agtgccaaac agcggcagtgtg ta 42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 62
 ccagtccgt gacaagcccc aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
 cccagaagtt caagggccccc cggcctcctg cgctcctgcc gcccggaccc tcgacacct 60
 cagagcagcc ggctgcgcgc cccggaaat ggcgaggagg agccgcacc gcctccctct 120
 gctgctgctg cgctacactgg tggtcgcctt gggctatcat aaggcctatg gttttctgc 180
 cccaaaagac caacaagtag tcacagcagt agagtaaaaa gaggctattt tagcctgcaa 240
 aaccccaaaag aagactgttt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300
 ctgttgcatac tatcaacaga ctcttcaagg tgatttaaa aatcgagctg agatgataga 360
 tttaaatatc cggatcaaaa atgtgacaag aagtgtatgcg gggaaatatc gttgtgaagt 420
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaaagtatt 480
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 gctcacgcct gtaatcccag cacttggaa ggccgcggcg ggcggatcac gaggtcagga 1020
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 acccggggagg cggagggttgc agtgagctga gatcacgcca ctgcagttca gcctggtaa 1200
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 tgtagaattt ttacaataaa tatagttga tattc 1295

<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
 Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45

Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95

Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110

Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190

Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205

Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220

Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240

Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255

Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270

Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe

305 310

<210> 65
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 65
atcgttgtga agttagtgcc cc 22

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 66
acctgcgata tccaacagaa ttg 23

<210> 67
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 67
ggaagaggat acagtcaactc tggaagtatt agtggctcca gcagttcc 48

<210> 68
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 68
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agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120
gcatcatgct gctattcctg caaatactga agaagcatgg gattaaata ttttacttct 180
aaataaaatga attactcaat ctcctatgac catctataca tactccacat taaaaaaatgt 240
catcaatatt atatcattaa gaaaaatgtt accttctttt ctccaaatatg catgacattt 300
ttggacaatg caattgtggc actggcactt atttcagtgtt agaaaaactt tttttttttt 360
tggcattcat catttgacaa atgcaagcat cttccatatac aatcagctcc tattgttactt 420
actagcactg actgtggat ctttaaggcc ccattacatt tctgttggaaag aaagctaaaga 480
tqaaggacat gcaactccga attcatgtgc tactttggcct agctatcact acacttagac 540

aagctgtaga taaaaaagtg gattgtccac gtttatgtac gtgtgaaatc aggccttgg 600
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 atgtgaggaa ttacttacag aaaccaaccc ttgcatttagg tgagctttat ctcctctga 2520
 taaatctctg ggaagcagaa aaagaaaaaa gtacatcaat gaaagtaaaa gcaactgtta 2580
 taggttacc aacaaatatc tcctaaaaac caccaaggaa acctactcca aaaaatgaac 2639

<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

Met	Lys	Asp	Met	Pro	Leu	Arg	Ile	His	Val	Leu	Leu	Gly	Leu	Ala	Ile
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Thr	Thr	Leu	Val	Gln	Ala	Val	Asp	Lys	Lys	Val	Asp	Cys	Pro	Arg	Leu	
														20	25	30

Cys	Thr	Cys	Glu	Ile	Arg	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Ile	Tyr	Met	
														35	40	45

Glu	Ala	Ser	Thr	Val	Asp	Cys	Asn	Asp	Leu	Gly	Leu	Leu	Thr	Phe	Pro	
														50	55	60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Gln Thr Asn Asn
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
480		
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
560		
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Asn	Thr	Thr	Thr	Leu	Met	Ala	Cys	Leu	Gly	Gly	Leu	Leu	Gly	Ile	Ile
625					630					635					640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
 660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70
<211> 1305
<212> DNA
<213> *Homo sapiens*

<400> 70
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ttaccacgct tggtggagta gatgaggaat gggctcgta ttatgctgac attccagcat 180
gaatctggta gacctgtggc taaccctgttc cctctccatg tgtctccccc tacaaagtt 240
tggttcttatg atactgtgct ttcatttgc cagtagtgtgt cccaaaggct gtctttgttc 300
ttccctctggg gggtttaaatg tcacctgttag caatgcaaat ctcaaggaaa tacctagaga 360
tcttcctccct gaaacagtct tactgtatct ggactccaat cagatcacat ctattccccaa 420
tgaaaattttt aaggacctcc atcaactgtag agttctcaac ctgtccaaaaa atggcattga 480
gtttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttgtc 540
cgacaatcgg attcaaagtg tgccaaaaaa tgccctcaat aacctgaagg ccagggccag 600
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cctgccaagc aggcagaaga aagcagatga acctgtatgtt attagcactg tggtagatgt 960
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cacccttaa ttgtacccccc gatggtatat ttctgagttaa gctactatct gaacattaaatg 1200
tagatccatc tcactattta ataatgaaat ttatttttt aattttaaaag caaataaaaag 1260
cttaactttg aaccatggga aaaaaaaaaaa aaaaaaaaaaa aaaca 1305

<210> 71
<211> 259
<212> PRT
<213> Hym

<100> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
 1 5 10 15

Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
 20 25 30

Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45

Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60

Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80

Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205

Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220

Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240

Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser
 245 250 255

Thr Val Val

<210> 72
 <211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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 attatggatt ttatgaaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
 aaaaaaaaaa 2290

<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
 20 25 30

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445

Asp Gly Asp Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser		
595	600	605
Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile		
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<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 74		
tcacctggag cctttattgg cc		22
<210> 75		
<211> 23		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 75		
ataccagcta taaccaggct gcg		23
<210> 76		
<211> 52		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 76		
caacagtaag tggtttgatg ctcttccaaa tcttagagatt ctgatgattg		50
gg		52
<210> 77		
<211> 22		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		

<400> 77
 ccatgtgtct ctcctacaa ag 22

 <210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 78
 gggaaatagat gtgatctgat tgg 23

 <210> 79
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 79
 cacctgttagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg 50

 <210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 80
 agcaaccgcc tgaagctcat cc 22

 <210> 81
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 81
 aaggcgccgtt gaaagatgtt gacg 24

 <210> 82

<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 82
gactacatgt ttcaggacct gtacaacctc aagtcaactgg aggttggcga 50

<210> 83
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 83
cccacgcgtc cgcacacctgg cccccgggctc cgaagcggtc cggggggcgcc ctttcggtca 60
acatcgtagt ccacccccc cccatccccca gccccccgggg attcaggctc gccagcgccc 120
agccagggag ccggccggga agcgcgtatgg gggccccagc cgcctcgctc ctgctcctgc 180
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aaaca 1685

<210> 84
<211> 398
<212> PRT
<213> Homo sapiens

<400> 84

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 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 20 25 30
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
 290 295 300
 Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
 305 310 315 320
 Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
 325 330 335
 Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
 340 345 350
 His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
 355 360 365
 Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
 370 375 380
 Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
 385 390 395

<210> 85
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 85
 gcttaggaatt ccacagaagc cc 22

<210> 86
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 86
 aacctggaat gtcaccgagc tg 22

<210> 87
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 87		
cctagcacag tgacgaggga cttggc		26
<210> 88		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 88		
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc		50
<210> 89		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 89		
gccctggcag acgagggcga gtacacctgc tcaatttca ctatgcgtgt		50
<210> 90		
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<212> DNA		
<213> Homo sapiens		
<400> 90		
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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 20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
65 70 75 80

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His			
100	105	110	
Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly			
115	120	125	
Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp			
130	135	140	
Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile			
145	150	155	160
Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr			
165	170	175	
Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu			
180	185	190	
Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu			
195	200	205	
Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys			
210	215	220	
Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val			
225	230	235	240
Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr			
245	250	255	
Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro			
260	265	270	
Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr			
275	280	285	
Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala			
290	295	300	
Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg			
305	310	315	320
Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala			
325	330	335	
Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly			
340	345	350	
Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala			
355	360	365	
Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp			
370	375	380	

Asn	Lys	Ile	His	Ser	Ile	Arg	Lys	Ser	His	Phe	Val	Asp	Tyr	Lys	Asn
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Leu	Ile	Leu	Leu	Asp	Leu	Gly	Asn	Asn	Ile	Ala	Thr	Val	Glu	Asn	
				405					410				415		
Asn	Thr	Phe	Lys	Asn	Leu	Leu	Asp	Leu	Arg	Trp	Leu	Tyr	Met	Asp	Ser
				420					425				430		
Asn	Tyr	Leu	Asp	Thr	Leu	Ser	Arg	Glu	Lys	Phe	Ala	Gly	Leu	Gln	Asn
				435				440				445			
Leu	Glu	Tyr	Leu	Asn	Val	Glu	Tyr	Asn	Ala	Ile	Gln	Leu	Ile	Leu	Pro
				450			455				460				
Gly	Thr	Phe	Asn	Ala	Met	Pro	Lys	Leu	Arg	Ile	Leu	Ile	Leu	Asn	Asn
				465			470			475				480	
Asn	Leu	Leu	Arg	Ser	Leu	Pro	Val	Asp	Val	Phe	Ala	Gly	Val	Ser	Leu
				485				490					495		
Ser	Lys	Leu	Ser	Leu	His	Asn	Asn	Tyr	Phe	Met	Tyr	Leu	Pro	Val	Ala
				500				505				510			
Gly	Val	Leu	Asp	Gln	Leu	Thr	Ser	Ile	Ile	Gln	Ile	Asp	Leu	His	Gly
				515				520				525			
Asn	Pro	Trp	Glu	Cys	Ser	Cys	Thr	Ile	Val	Pro	Phe	Lys	Gln	Trp	Ala
				530			535				540				
Glu	Arg	Leu	Gly	Ser	Glu	Val	Leu	Met	Ser	Asp	Leu	Lys	Cys	Glu	Thr
				545			550			555				560	
Pro	Val	Asn	Phe	Phe	Arg	Lys	Asp	Phe	Met	Leu	Leu	Ser	Asn	Asp	Glu
				565				570				575			
Ile	Cys	Pro	Gln	Leu	Tyr	Ala	Arg	Ile	Ser	Pro	Thr	Leu	Thr	Ser	His
				580				585				590			
Ser	Lys	Asn	Ser	Thr	Gly	Leu	Ala	Glu	Thr	Gly	Thr	His	Ser	Asn	Ser
				595				600				605			
Tyr	Leu	Asp	Thr	Ser	Arg	Val	Ser	Ile	Ser	Val	Leu	Val	Pro	Gly	Leu
				610			615				620				
Leu	Leu	Val	Phe	Val	Thr	Ser	Ala	Phe	Thr	Val	Val	Gly	Met	Leu	Val
				625			630			635				640	
Phe	Ile	Leu	Arg	Asn	Arg	Lys	Arg	Ser	Lys	Arg	Arg	Asp	Ala	Asn	Ser
				645				650				655			
Ser	Ala	Ser	Glu	Ile	Asn	Ser	Leu	Gln	Thr	Val	Cys	Asp	Ser	Ser	Tyr

660	665	670
Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp		
675	680	685
Cys Gly Ser His Ser Leu Ser Asp		
690	695	
<210> 92		
<211> 22		
<212> DNA		
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<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 92		
gttggatctg ggcaacaata ac		22
<210> 93		
<211> 24		
<212> DNA		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 93		
attgttgtgc aggctgagtt taag		24
<210> 94		
<211> 45		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 94		
ggtggctata catggatagc aattacctgg acacgctgtc ccggg		45
<210> 95		
<211> 2226		
<212> DNA		
<213> Homo sapiens		
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agtgcactgc gtccctgtta cccggcgcca gctgtgttcc tgaccccaga ataactcagg		60
gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgccggctaa gggaaaactgt		120
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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
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Gly Pro Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80
 Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
 100 105 110
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

Ser	Thr	Met	Ser	Thr	Leu	Gln	Met	Ser	Leu	Gln	Ala	Glu	Ser	Lys	Ala	340	345	350
																355	360	365
Thr	Ile	Thr	Pro	Ser	Gly	Ser	Val	Ile	Ser	Lys	Phe	Asn	Ser	Thr	Thr	370	375	380
																385	390	395
Ser	Ser	Ala	Thr	Pro	Gln	Ala	Phe	Asp	Ser	Ser	Ser	Ala	Val	Val	Phe			
																400		
Ile	Phe	Val	Ser	Thr	Ala	Val	Val	Val	Leu	Val	Ile	Leu	Thr	Met	Thr	405	410	415
Val	Leu	Gly	Leu	Val	Lys	Leu	Cys	Phe	His	Glu	Ser	Pro	Ser	Ser	Gln			
																420	425	430
Pro	Arg	Lys	Glu	Ser	Met	Gly	Pro	Pro	Gly	Leu	Glu	Ser	Asp	Pro	Glu			
																435	440	445
Pro	Ala	Ala	Leu	Gly	Ser	Ser	Ser	Ala	His	Cys	Thr	Asn	Asn	Gly	Val			
																450	455	460
Lys	Val	Gly	Asp	Cys	Asp	Leu	Arg	Asp	Arg	Ala	Glu	Gly	Ala	Leu	Leu			
																465	470	475
Ala	Glu	Ser	Pro	Leu	Gly	Ser	Ser	Asp	Ala									
																485	490	

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<210> 97  
<211> 24  
<212> DNA  
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97
tggaaggaga tgcgatgccca cctg

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<210> 98
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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<400> 98
tgaccqaqtqq qqaaggacag 20

<210> 99		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 99		
acagagcaga gggtgcccttg		20
<210> 100		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 100		
tcagggacaa gtggtgtctc tccc		24
<210> 101		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 101		
tcagggaaagg agtgtgcagt tctg		24
<210> 102		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 102		
acagctcccc atctcagttt cttgcattgc ggacgaaatc ggcgctcgct		50
<210> 103		
<211> 2026		
<212> DNA		
<213> Homo sapiens		

<400> 103

cggacgcgtg ggattcagca gtggactgtg gtcgtccagag cagtcctca ggggaaacta 60
 agcgtcgagt cagacggcac cataatcgcc tttaaaatgt cctccgcctt gcccggcg 120
 tatccccgg ctacctgggc cgccccggcg cggtgccgcgt gtgagaggga gcgcgcggc 180
 agccgagcgc cggtgtgagc cagcgtctgtc gocagtgta gcggcggtgt gagcgcggtg 240
 ggtgcggagg ggcgtgtgt ccggcgcgcg cgccgtgggg tgcaaacccc gagcgtctac 300
 gctgccatga ggggcgcgaa cgcctggcg ccactctgcc tgctgctggc tgccgcacc 360
 cagctctcgcc ggcagcagtc cccagagaga cctgtttca catgtggtgg cattcttact 420
 ggagagtctg gatttattgg cagtgaaggt ttcctggag tgtaccctcc aaatagcaaa 480
 tgtacttggaa aatcacagt tcccaagga aagtagtgc ttctcaattt ccgattcata 540
 gacctcgaga gtgacaacct gtgccgtat gactttgtgg atgtgtacaa tggccatgcc 600
 aatggccagc gcattggccg cttctgtggc actttccgcg ctggagccct tgggtccagt 660
 ggcaacaaga tggatggcgtca gatgatttct gatgccaaca cagctggcaa tggcttcatg 720
 gccatgttct ccgctgtga accaaacgaa agaggggatc agtattgtgg aggactccctt 780
 gacagacattt ccggctcttt taaaaccccc aactggccag accgggattt ccctgcagga 840
 gtcacttggtg tggcgttcat tggatggccat aagaatcagc ttatagaatt aaagtttgag 900
 aagtttgatg tggagcgaga taactactgc cgatatgattt atgtggctgt gtttaatggc 960
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 actgtgtcca tttaagctgtt attctgtccat tgcctttgaa agatctatgt tctctcagta 1620
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 ctaaaagtgtt caagcgttga cagcttggaa gcgtttatattt atacatctt gtaaaaggat 1860
 attttagaat tgagttgtgt gaagatgtca aaaaaagattt ttagaagtgc aatatttata 1920
 gtgttatttg ttccaccttc aagcccttgc cctgaggtgt tacaatcttgc tcttgcgttt 1980
 tctaaatcaa tgcttaataa aatattttta aaggaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met	Arg	Gly	Ala
1	5	10	15

Ala	Thr	Gln	Leu
20	25	30	

Cys	Gly	Gly	Ile
35	40	45	

Phe	Pro	Gly	Val
50	55	60	

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Leu Leu Asp Arg
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270

Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
-----	-----	-----

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
 355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
 370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
 385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
 405 410 415

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 105
ccgattcata gacctcgaga gt 22

<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 106
gtcaaggagt cctccacaat ac 22

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 107
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45
<210> 108
<211> 1838
<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg ggcggacgcg tggcgccccc acggcgcccg cgggctgggg cggtcgcttc 60
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 aaggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
 atctggctcc agccctctcc acctccccag tcttctcccc cgcctcagcc ccatccgtgt 240
 catacctgcc ggggactggg tgacagcttt aacaaggccc tggagagaac catccggac 300
 aactttggag gtggaaacac tgcctggag gaagagaatt tgtccaaata caaagacagt 360
 gagaccggcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgcac 420
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 gccccggacc tcttccagtg gctgtgctca gattccctga agctctgtg ccccgccaggc 540
 accttcgggc ctcctgcct tccctgtcct gggggAACAG agaggccctg cggtggtac 600
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 tcaaactgtt tgcaatgcaa gaagggtctgg gcccctgcattt acctcaagtg tgttagacatt 840
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 ggctccatag agtgccgaga ctgtgccaag gcctgcctag gctgcattggg ggcagggcca 960
 ggtcgtgtt agaagtgttag ccctggctat cagcaggtgg gctccaagtg tctcgatgtg 1020
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 cagcagatgt tcttggcat catcatctgt gcactggcca cgctggctgc taagggcgac 1260
 ttggtgttca ccgcattt cattggggct gtggcggcca tgactggcta ctgggtgtca 1320
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 gataccatga gctttcacc tggcggggac tggcaggctt cacaatgtgtt gaatttcaaa 1620
 agttttccct taatggtggc tgctagagct ttggccctt cttaggatta ggtggcctc 1680
 acaggggtgg ggccatcaca gtccttcctt gccagctgca tgctgccagt tcctgttctg 1740
 tgttcaccac atccccacac cccattgcca cttattttt catctcagga aataaaagaaa 1800
 ggtctggaa agttaaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met	Ala	Pro	Trp	Pro	Pro	Lys	Gly	Leu	Val	Pro	Ala	Val	Leu	Trp	Gly
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Leu	Ser	Leu	Phe	Leu	Asn	Leu	Pro	Gly	Pro	Ile	Trp	Leu	Gln	Pro	Ser
20															

Pro	Pro	Pro	Gln	Ser	Ser	Pro	Pro	Pro	Gln	Pro	His	Pro	Cys	His	Thr
35															

Cys	Arg	Gly	Leu	Val	Asp	Ser	Phe	Asn	Lys	Gly	Leu	Glu	Arg	Thr	Ile
50															

Arg	Asp	Asn	Phe	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Glu	Asn	Leu	
65										75				80	
Ser	Lys	Tyr	Lys	Asp	Ser	Glu	Thr	Arg	Leu	Val	Glu	Val	Leu	Glu	Gly
				85						90				95	
Val	Cys	Ser	Lys	Ser	Asp	Phe	Glu	Cys	His	Arg	Leu	Leu	Glu	Leu	Ser
					100				105				110		
Glu	Glu	Leu	Val	Glu	Ser	Trp	Trp	Phe	His	Lys	Gln	Gln	Glu	Ala	Pro
				115				120				125			
Asp	Leu	Phe	Gln	Trp	Leu	Cys	Ser	Asp	Ser	Leu	Lys	Leu	Cys	Cys	Pro
					130			135			140				
Ala	Gly	Thr	Phe	Gly	Pro	Ser	Cys	Leu	Pro	Cys	Pro	Gly	Gly	Thr	Glu
					145			150			155			160	
Arg	Pro	Cys	Gly	Gly	Tyr	Gly	Gln	Cys	Glu	Gly	Glu	Gly	Thr	Arg	Gly
					165				170			175			
Gly	Ser	Gly	His	Cys	Asp	Cys	Gln	Ala	Gly	Tyr	Gly	Glu	Ala	Cys	
					180				185			190			
Gly	Gln	Cys	Gly	Leu	Gly	Tyr	Phe	Glu	Ala	Glu	Arg	Asn	Ala	Ser	His
				195			200			205					
Leu	Val	Cys	Ser	Ala	Cys	Phe	Gly	Pro	Cys	Ala	Arg	Cys	Ser	Gly	Pro
				210			215			220					
Glu	Glu	Ser	Asn	Cys	Leu	Gln	Cys	Lys	Lys	Gly	Trp	Ala	Leu	His	His
					225			230			235			240	
Leu	Lys	Cys	Val	Asp	Ile	Asp	Glu	Cys	Gly	Thr	Glu	Gly	Ala	Asn	Cys
					245				250			255			
Gly	Ala	Asp	Gln	Phe	Cys	Val	Asn	Thr	Glu	Gly	Ser	Tyr	Glu	Cys	Arg
					260				265			270			
Asp	Cys	Ala	Lys	Ala	Cys	Leu	Gly	Cys	Met	Gly	Ala	Gly	Pro	Gly	Arg
					275			280			285				
Cys	Lys	Lys	Cys	Ser	Pro	Gly	Tyr	Gln	Gln	Val	Gly	Ser	Lys	Cys	Leu
					290			295			300				
Asp	Val	Asp	Glu	Cys	Glu	Thr	Glu	Val	Cys	Pro	Gly	Glu	Asn	Lys	Gln
					305			310			315			320	
Cys	Glu	Asn	Thr	Glu	Gly	Gly	Tyr	Arg	Cys	Ile	Cys	Ala	Glu	Gly	Tyr
					325				330			335			
Lys	Gln	Met	Glu	Gly	Ile	Cys	Val	Lys	Glu	Gln	Ile	Pro	Glu	Ser	Ala
					340			345			350				

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgt agccctcgac ac

22

<210> 113

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113

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tgagaccctc ctgcagcctt ctcaaggac agccccactc tgccctttgc tcctccaggg 60
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cggggccgccc ctgaccgggg agcagctcct gggcagcctg ctgcggcage tgcagctcaa 180
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gcggctttc caggagccgg tcccaaggc cgccgtgcac aggacacggc ggctgtcccc 480
gcgcagcgcgc cggggccggg tgaccgtcga gtggctgcgc gtccgcgcac acggctccaa 540
ccgcacccctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggccct 600
cgacgtgacc gaggccgtga acttctggca gcaagctgagc cggcccccggc agccgctgct 660
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aaagtccctcc accaccactc tggacctaag acctgggggt aagtgtgggt tgtgcacccc 1560
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<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114

Met	Gln	Pro	Leu	Trp	Leu	Cys	Trp	Ala	Leu	Trp	Val	Leu	Pro	Leu	Ala
1															

Ser	Pro	Gly	Ala	Ala	Leu	Thr	Gly	Glu	Gln	Leu	Leu	Gly	Ser	Leu	Leu
20															

Arg	Gln	Leu	Gln	Leu	Lys	Glu	Val	Pro	Thr	Leu	Asp	Arg	Ala	Asp	Met
35															

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 115

aggactgcc a taacttgccct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 116

ataggagttg a a g c a g c g c t g c

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

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 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180

aatcctgtga agttgtcctg tgcctactcg ggctttctt ctccccgtgt ggagtggaaag 240
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 tcaaatgctg tgcgcatgga agctgtggag cgaaatgtgg gggtcatcgt ggcagccgtc 780
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 agtgcggaa gtgaaggaga attcaaacag acctcgcat tcctgggtg agcctggtcg 960
 gctcaccgccc tatcatctgc atttgcctta ctcagggtct accgactct gggccctgat 1020
 gtctgttagtt tcacaggatg ctttacacc ccacagggcc ccctacttct 1080
 tcggatgtgt ttttaataat gtcagctatg tgccccatcc tccttcatgc cctccctccc 1140
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<210> 119
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 119															
Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe	Ile
1															15
Leu	Ala	Ile	Leu	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr	Val	His
20															30
Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro	Val	Lys	Leu
35															45
Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val	Glu	Trp	Lys	Phe
50															60
Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asn	Asn	Lys	Ile	Thr
65															80
Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu	Pro	Thr	Gly	Ile	Thr	Phe
85															95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly
 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tgcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 121
 tgatcgcgtt gggcacaaag gcgcaagctc gagagggaaac ttttgtgcct 50

<210> 122
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 122
 acacacctggttt caaaggatggg 20

<210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 123
 taggaagagt tgctgaaggc acgg 24

<210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 124
 ttgccttact caggtgctac 20

<210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 125		
actcagcagt ggttagaaag		20
<210> 126		
<211> 1210		
<212> DNA		
<213> Homo sapiens		
<400> 126		
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gctcaggctc gtgcccaccc accaagttcc agtgcgcac cagtggctta tgcgtgcccc 240		
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300		
ggattgagcc atgtacccag aaagggaat gcccaccggc ccctggcctc ccctgcctt 360		
gcacccgcgt cagtgaactgc tctggggaa ctgacaagaa actgcgcac ac 420		
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480		
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aagttgttc		1210
<210> 127		
<211> 282		
<212> PRT		
<213> Homo sapiens		
<400> 127		
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Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu		
20 25 30		
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly		
35 40 45		
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser		
50 55 60		
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys		
65 70 75 80		

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95

Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 128

aagttccagt gcccaccaag tggc

24

<210> 129

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 129
ttggttccac agccgagtc gtcg 24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc 50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cggtctcgct cgctcgca gggcgccag cagaggtcgc gcacagatgc 60
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cagactcttg caagctggat gcccctgtg gatgaaagat gtatcatgga atgaaccgga 180
gcaatggaga tggatttcta gagcagcgcg acgagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgtatcgt tggttcagc tggcgctgtg ctccggccct gcacagctca 300
cgggcggtt cgatgacctt caagtgtgtg ctgacccccc cattcccgag aatggctca 360
ggaccccccag cggaggggtt ttcttgaag gctctgtgc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgtc acaaagagac ttttttttgc gatattaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgcgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaattt atcacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat gtttcatta tgtcgcgtatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcgt gacaccccta gcctcttcta 720
atggctatgt aaacatctt gagtcacggc cctccttccc ggtggggact gtgtatcttctt 780
atcgctgttt tcccggtt aaacctgtt ggtctgtgtc tcttgagtgc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgtctgtga agcccaagtc tgtccactac 900
ctccaaatggt gagtcacggc gatgtgttgc gcccacccgcg gcctgtgag cgctacaacc 960
acggaactgt ggtggagtt tactgcgtc ctggctacag cctcaccaggc gactacaagt 1020
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 ctcccagggtg ccaagagagc acccaccctg ctccggacaa ccctgacata attgccagca 1560
 cgccagagga ggtggcatcc accagccccag gcatccatca tgcccaactgg gtgttgttcc 1620
 taagaaactg attgattaaa aaatttccca aagtgtccctg aagtgtctct tcaaatacat 1680
 gttgatctgt ggagttgatt ctttccttc tcttggttt agacaaatgt aaacaaagct 1740
 ctgatcccta aaattgctat gctgatagag tggtagggc tggaaagctt atcaagtcc 1800
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
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Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
20														30

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
35														45	

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
50														60	

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65														80	

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
85														95	

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
100														110	

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
115														125	

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
130														140	

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
145														160	

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
165														175	

Cys	Gln	Gly	Cys	Leu	Arg	Pro	Leu	Ala	Ser	Ser	Asn	Gly	Tyr	Val	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133
atctcctatac gctgctttcc cgg 23

<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134
agccaggatc gcagtaaaac tcc 23

<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135
atttaaac tt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens

<400> 136
cccacgcgtc cgctccgcgc cctccccccc gcctcccggt cggtccgtcg gtggccataga 60
gatgctgctg ccgcgggtgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
ccgttagcgcc cgagtgtcg ggccgcacc cgagtccggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgctggcc gtgctgtgg tggggctgcg ggcgcgcacg ggtcgcctgc 240
tgagtgcctc gatattggac ctcagaggag ggcagccagt ctgcggggga gggacacaga 300

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

<211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 138
 gttcattgaa aaccttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 139
 aagccaaaga agcctgcagg aggg 24

<210> 140
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 140
 cagtccaaagc ataaaggtcc tggc 24

<210> 141
 <211> 1514
 <212> DNA
 <213> Homo sapiens

<400> 141
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaagg ctggatgtac 60
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 ttgtgtttgc ctccctgcagc ctcaacccgg agggcagcga gggctacca ccatgatcac 180
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 tcctctcaag ccgctccgc tggaggagca ggttagagtgg aaccggcagc tattagaggt 420
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qcctttatac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
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Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
 115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190

Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
 385 390 395 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
 405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425

<210> 143
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143
ccaaactacca aagctgctgg agcc 24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 144
gcagctctat taccacggga agga 24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145
tccttccccgt ggtaatagag ctgc 24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg 45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttcttagc 60
cttaaatttc agctcatcac cttcacctgc cttggtcatg gctctgctat ttccttttat 120
ccttqccatt tqcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggg 180

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
gtgtatgac ggctgggaca ttaaggacgt ggctgtgtt tgccggagc tggctgtgg 300
agctgccagc ggaaccccta gtgttatttt gtatgagcca ccagcagaaa aagagcaaaa 360
ggtcctcatc caatcagtca gttgcacagg aacagaagat acattggctc a诶gtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcggtg a诶gaacccaga 480
gagctcttc tccccagtc cagagggtgt caggctggc gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtgttatacc gtgtgccaga caggctggag 600
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aaaacgctgc aacaaggcatg cctatggccg aaaaccatc tggctgagcc agatgtcatg 720
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cattctcaca cacacacacaca cacacacacaca cacacataca ccattgtcc 1500
tgtttctctg aagaactctg acaaataca gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat ttctgtattt gtttatgggg ttctgtaaat tggctctata 1620
atctaatttag atataaaatt ctggtaactt tatttacaat aataaaagata gcaactatgt 1680
ttcaaa

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
 1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
 20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
 65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
 100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149		
ttcagctcat caccttcacc tgcc		24
<210> 150		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 150		
ggctcataca aaataccact aggg		24
<210> 151		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 151		
gggcctccac cgctgtgaag ggccgggtgaa ggtggAACAG aaaggCCAGT		50
<210> 152		
<211> 1427		
<212> DNA		
<213> Homo sapiens		
<400> 152		
actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgcaccc 60 acccacgcgt cccggacgc gtgggggac gcgtggggcg gctaccagga agagtctgcc 120 gaaggtgaag gccatggact tcatacaccc cacagccatc ctgcggctgc tggtcggtcg 180 cctggcgctc ttccggctct tccggctgct gcagtgggtg cgcgggaagg cctacctgcg 240 aatgtgtg tggtgtatca caggccac ctccggctg ggcaagaat gtgcaaaagt 300 cttctatgtc gccccgtcta aactgggtct ctgtggccgg aatgggtgggg ccctagaaga 360 gctcatcaga gaacttaccc ttctcatgc caccaagggtg cagacacaca agccttactt 420 ggtaaccttc gacccatcacag actctggggc catagttgca gcagcagctg agatcctgca 480 gtgtttggc tatgtcgaca tacttgtcaa caatgtggg atcagctacc gtggtaccat 540 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccaagt 600 tgctctaaccg aaaggactcc tgccctccat gatcaagagg aggoaaggcc acattgtcg 660 catcaggcgc atccaggcga agatgagcat tcctttcga tcagcatatg cagcctccaa 720 gcacgcaacc caggcttct ttgactgtct gcgtggcgag atggaaacagt atgaaaattga 780 ggtaaccttc atcagcccg gctacatcca caccaaccc tctgtaaatg ccatcacccgc 840 ggatggatct aggtatggag ttatggacac caccacagcc caggccgaa gccctgtgaa 900 ggtggcccaag gatgttctg ctgtgtgggg gaagaagaag aaagatgtga tctggctga 960 cttactgcct tccttggctg tttatctcg aactctggct cctggccctct tcttcaggct 1020 catggccctcc agggccagaa aagagcggaa atccaagaac tccttagtact ctgaccagcc 1080		

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 ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaaca 1320
 tctcaaacag taaaaaaaaaaa aaaaaagggc gcgcgcact ctagagtcga cctgcagaag 1380
 cttggccgccc atggcccaac ttgttattt cagttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met	Asp	Phe	Ile	Thr	Ser	Thr	Ala	Ile	Leu	Pro	Leu	Leu	Phe	Gly	Cys
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Leu	Gly	Val	Phe	Gly	Leu	Phe	Arg	Leu	Leu	Gln	Trp	Val	Arg	Gly	Lys
															30
		20					25								

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
															45
		35					40								

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
															60
		50				55									

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
															80
		65				70				75					

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
															95
		85				90									

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	
															110
		100				105									

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
															125
		115				120									

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
															140
		130			135										

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
															160
		145			150					155					

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
															175
		165			170										

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
															190
		180			185										

Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
															205
		195			200										

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg		
225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu		
245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val		
260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu		
275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu		
290	295	300
Arg Lys Ser Lys Asn Ser		
305	310	

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154

ggtgctaaac tggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156
 tcatactgtt ccatctcggc acgc 24

 <210> 157
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 157
 aatgggtgggg ccctagaaga gctcatcaga gaactcacccg cttctcatgc 50

 <210> 158
 <211> 1771
 <212> DNA
 <213> Homo sapiens

 <400> 158
 cccacgcgtc cgctgggtt agatcgagca accctctaaa agcagttag agtgtaaaa 60
 aaaaaaaaaa acacaccaaa cgctcgacg cacaaggatc atgaaatttc ttctggacat 120
 cctcctgtt ctcgggttac tgatcgctg ctccctagag tccttcgtga agcttttat 180
 tcctaagagg agaaaatca gtcaccggcga aatcgctgtt attacaggag ctgggcattgg 240
 aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
 tataaataag catggactgg aggaaacagc tgccaaatgc aaggactgg gtgccaagg 360
 tcataccctt gtggtagact gcagcaaccc agaagatatt tacagctgtt caaagaagg 420
 gaaggcagaa attggagatg ttagtatttt agtaaataat gctgggttag tctatacatc 480
 agattttttt gtcacacaag atcctcagat tgaaaagact tttgaagttt atgtacttgc 540
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 tgtcaactgtt gcttcggcag ctggacatgt ctgggtcccc ttcttactgg cttaactgtt 660
 aagcaagttt gctgctgtt gatttcataa aactttgaca gatgaactgg ctgccttaca 720
 aataactgga gtcaaaacaa catgtctgtt tcctaatttc gtaaacactg gcttcatcaa 780
 aaatccaagt acaagtttgg gacccactct ggaaccttag gaagtggtaa acaggctgt 840
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 aacattggaa aggttccttc ctgagcgtt ctggcagg ttaaaacgaa aaatcagtgt 960
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1771

<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
1															

5

10

15

Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
20							25					30			

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
35							40				45				

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
50						55				60					

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
65						70			75		80				

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
85						90					95				

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
100						105					110				

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
115						120					125				

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
130						135				140					

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
145						150				155		160			

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
165						170					175				

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
180						185					190				

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
195						200					205				

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
210						215					220				

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
225						230				235		240			

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
245						250					255				

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 161

atccccatgca tcagcctgtt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 162

gctgggttag tctatacatc agatttgttt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgccggacgcg tgggtcgact agttctagat cgccgagcggc cgccccggc 60
 tcaggagga gcaccgactg cgccgcaccc tgagagatgg ttgggtgccat gtggaaaggtg 120

attgttcgc tggcctgtt gatgcctggc ccctgtatg ggctgttcg ctccctatac 180
 agaagtgtt ccatgccacc taaggagac tcaggacagc cattatttct cacccttac 240
 attgaagctg ggaagatcca aaaagaaga gaatttagtt tggcggccc ttcccagga 300
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaaccc 360
 ttcttcgtt tttcccaggc tcagatacag ccagaagatg ccccactgt tctctggcta 420
 cagggtggc cgggagggttc atccatgtt ggactcttg tggaacatgg gccttatgtt 480
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
 ctttacattg acaatccagt gggcacagcc ttcagtttta ctgtgatac ccacggatat 600
 gcagtcataatg aggacgatgt agcacggat ttatacagtg cactaattca gttttccag 660
 atatccctg aatataaaaaa taatgactt tatgtcactg gggagtcata tgcaaggaaa 720
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
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 cattgctgaa aagaaaatcg taaaaacaga aatgtcata ggaataaaaaa aattatctt 1620
 tcataatctgc aagatttttt tcataataa aaattatctt tgaaacaatg gagctttgt 1680
 ttttgggggg agatgtttac tacaaaatta acatgagatc atgagtaaga attacattat 1740
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 gtgttggaa atattattgg ataagaatag ctcaattatc ccaaaataat ggtatgaaatc 1980
 ataatagtt tggggaaaag attctcaaattt gtaataagtc ttggaaacaaa agaattctt 2040
 gaaataaaaaa tattatataat aaaagtaaaa aaaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1									10					15	

Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	Arg	Ser	Leu	Tyr	Arg	Ser	Val	Ser
20									25					30	

Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
35									40					45	

Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
50										55				60	

Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Gly	Phe	Leu	Thr	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Pro Ala Gln			
85	90	95	
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100	105	110	
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115	120	125	
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130	135	140	
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145	150	155	160
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165	170	175	
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180	185	190	
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195	200	205	
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210	215	220	
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225	230	235	240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245	250	255	
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His			
260	265	270	
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275	280	285	
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290	295	300	
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305	310	315	320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325	330	335	
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340	345	350	

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
405 410 415

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 165
ttccatgcca cctaagggag actc 24

```
<210> 166
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 166
tggatgaggt gtgcaatggc tggc 24

<210> 167
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167
agctctcaga ggctggtcat aggg 24

<210> 168
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 168
gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac 50

<210> 169
<211> 2477
<212> DNA
<213> Homo sapiens

<400> 169
cgagggcttt tccggctccg gaatggcaca tgtggaaatc ccagtcttgt tggctacaac 60
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tcttgcgttga gaagaaaagggt ctgagggcag agcagggcac tctcaactcag ggtgaccagc 180
tccttgcctc tctgtggata acagagcatg agaaagtggaa gagatgcagc ggagtggagg 240
gatggaaagtc taaaatagga aggaattttg tgtcaatat cagactctgg gagcagttga 300
cctggagagc ctgggggagg gcctgcctaa caagcttca aaaaacagga gcgacttcca 360
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attgactggc tgggtgaact tcaacagcct ttaacacctc ctggggatg aaaacgatgg 480
cttaaggggc cagaaaataga gatgcttgc taaaataaaat ttaaaaaaaaa gcaagtattt 540
tatagcataa aggctagaga ccaaaaataga taacaggatt ccctgaacat tcctaagagg 600
gagaaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660
accaggatgg ggaccctggg tcagggccagc ctcttgcctc ctcccgaaaa ttatTTTGG 720
tctgaccact ctgccttgc tttgcagaa tcatgtgagg gccaaccggg gaaggtggag 780
cagatgagca cacacaggag ccgtctcctc accggccccc ctctcagcat ggaacagagg 840
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 aggggttaat ttgtgactt agcttctagc tacttcctcc agccatcagt cattgggtat 2400
 gtaaggaatg caagcgtatt tcaatatttc ccaaacttta agaaaaaaact ttaagaaggt 2460
 acatctgcaa aagcaaa 2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met	Gly	Thr	Leu	Gly	Gln	Ala	Ser	Leu	Phe	Ala	Pro	Pro	Gly	Asn	Tyr
1			5					10				15			

Phe	Trp	Ser	Asp	His	Ser	Ala	Leu	Cys	Phe	Ala	Glu	Ser	Cys	Glu	Gly
							20		25				30		

Gln	Pro	Gly	Lys	Val	Glu	Gln	Met	Ser	Thr	His	Arg	Ser	Arg	Leu	Leu
							35		40			45			

Thr	Ala	Ala	Pro	Leu	Ser	Met	Glu	Gln	Arg	Gln	Pro	Trp	Pro	Arg	Ala
						50		55			60				

Leu	Glu	Val	Asp	Ser	Arg	Ser	Val	Val	Leu	Leu	Ser	Val	Val	Trp	Val
							65		70			75		80	

Leu	Leu	Ala	Pro	Pro	Ala	Ala	Gly	Met	Pro	Gln	Phe	Ser	Thr	Phe	His
							85		90			95			

Ser	Glu	Asn	Arg	Asp	Trp	Thr	Phe	Asn	His	Leu	Thr	Val	His	Gln	Gly
							100		105			110			

Thr	Gly	Ala	Val	Tyr	Val	Gly	Ala	Ile	Asn	Arg	Val	Tyr	Lys	Leu	Thr
							115		120			125			

Gly	Asn	Leu	Thr	Ile	Gln	Val	Ala	His	Lys	Thr	Gly	Pro	Glu	Glu	Asp
							130		135			140			

Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val
							145		150			155		160	

Leu	Thr	Leu	Thr	Asn	Asn	Val	Asn	Lys	Leu	Leu	Ile	Ile	Asp	Tyr	Ser
							165		170			175			

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

100

450 455 460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540
Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171

tggaaataccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173
 ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42

 <210> 174
 <211> 3106
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (1683)
 <223> a, t, c or g

 <400> 174
 aggctccgc gcggggctga gtgcggactg gagtggaaac ccgggtcccc ggcgttagag 60
 aacacgcgt gaccacgtgg agcctccggc ggaggccgc cgcacgcgt ggactcctgc 120
 tgctggtcgt ctgggcttc ctgggtctcc gcaggctgaa ctggagcacc ctggccctc 180
 tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240
 attccacccct ctggatcttc gggggctcca tccactattt ccgtgtgccg agggagtact 300
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 cgtggAACCT gcatgagccaa gaaagaggca aatttgactt ctctggaaac ctggacctgg 420
 aggccttcgt cctgtatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccct 480
 acatctgcag ttagatggac ctgggggct tgcccgatcg gctactccaa gaccctggca 540
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 tgatgtccag ggtgggtccaa ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660
 tggagaatga atatggttcc tataataaaag acccccgcata catgccctac gtcaagaagg 720
 cactggagga ccgtggcatt gtggaaactgc toctgacttc agacaacaag gatgggctga 780
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_{RES}

<222> (539)

<223> Any amino acid

<400> 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu
1				5					10					15	

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
85 90 95

Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser
							100				105			110	

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg agctgagagg ctccgggcta gctaggtgta ggggtggacg ggtccccagga 60
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 aaggggagca aagccgggct cggcccgagg ccccccaggac ctccatctcc caatgttgaa 180
 ggaatccgac acgtgacggt ctgtccggc ttcagacta gaggagcgct gtaaacgcca 240
 tggctcccaa gaagctgtcc tgcctcggt ccctgctgct gccgctcggc ctgacgctac 300
 tgctggccca ggcagacact cggtcgttcg tagtggata gggtcatgac cggtttctcc 360
 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

tgctttggc cgaccggc ttgaagatgc gatggagcgg cctcaacgcc atacagttt 480
atgtccctg gaactaccac gagccacagc ctggggctca taaccttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctggttg cticgaaaac 660
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tggctggct cttccgtca ctgctaggag aaaagatctt gctttcacc acagatggc 900
ctgaaggact caagtgtgg tccctccggg gactctatac cactgttagat tttggccag 960
ctgacaacat gaccaaatac tttacccctgc ttcggaga tgaacccat gggccattgg 1020
taaactctga gtactacaca ggctggctgg attactgggg ccagaatcac tccacacgg 1080
ctgtgtcagc tgtaacccaa ggactagaga acatgctcaa gttggagcc agtgtgaaca 1140
tgtacatgtt ccatggaggt accaactttg gatattggaa tggtgcgtat aagaaggac 1200
gcttccttcc gattactacc agctatgact atgatgcacc tatactgaa gcaggggacc 1260
ccacacctaa gcttttgc cttcgagatg tcatacggcaaa gttccaggaa gttcccttgg 1320
gaccttacc tcccccgagc cccaaatgta tgcttggacc tgtgactctg cacctggttg 1380
ggcatttact ggcttccta gacttgc tggccat gcccattcat tcaatcttgc 1440
caatgaccc ttgaggctgtc aagcaggacc atggctcat gttgtaccga acctatatga 1500
cccataccat ttttggcca acaccattct ggggtccaaa taatggagtc catgaccgtg 1560
cctatgtat ggtggatggg gtgtccagg gtgtgttgg ggcgaaatatg agagacaaac 1620
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ggtttccctt ccagttgcca aaatggccat atcctcaagc tcctctggc cccacattct 1860
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ggccacaaca gaccctctac gtgccaagat tcctgctgtt tcctagggga gcccctcaaca 2040
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agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
atacactgag tgcctctgaa ccaatggagt taagtggca ctgaaaggta ggcggggcat 2220
ggtggctcat gcctgtatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
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aaatttagccg ggcgtatgg tggcacctc taatcccagc tacttgggag gctgaggc 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggaggttgc accactgcac 2460
tccagctgg ctgacagtga gacactccat tcaaaaaaaaaaaa 2505

<210> 177
<211> 654
<212> PRT
<213> Homo sapiens

<400> 177
Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
1 5 10 15

Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
50 55 60

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
 65 70 75 80
 Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
 85 90 95
 Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
 100 105 110
 Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
 115 120 125
 Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
 130 135 140
 Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
 145 150 155 160
 Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
 165 170 175
 Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
 180 185 190
 Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
 195 200 205
 Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
 210 215 220
 Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro
 225 230 235 240
 Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
 245 250 255
 His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
 260 265 270
 Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
 275 280 285
 Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
 290 295 300
 His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
 305 310 315 320
 Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
 325 330 335
 Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
 645 650

<210> 178
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178
tggctactcc aagaccctgg catg 24

<210> 179
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 179
tggacaaaatc cccttgctca gccc 24

<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 180
gggcttcacc gaagcagtgg acctttatcc tgaccacctg atgtccaggg 50

<210> 181
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 181
ccagctatga ctatgtatgc cc 22

<210> 182
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182
 tggcacccag aatggtgttg gctc 24

<210> 183
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183
 cgagatgtca tcagcaagtt ccaggaagtt ctttggac cttaacctcc 50

<210> 184
 <211> 1947
 <212> DNA
 <213> Homo sapiens

<400> 184
 gcttgaaca cgctgcagg cccaaagttt agcatctgat tggtatgag gtattttagt 60
 gcaccacaa tatggcttac atgttaaaaa agcttctcat cagttacata tccattattt 120
 gtgttatgg ctttatctgc ctctacactc tcttctgggtt attcaggata ccttgaagg 180
 aatattctt cggaaaaagtc agagaagaga gcagtttag tgacattcca gatgtcaaaa 240
 acgattttgc gttccttctt cacatggtag accagttatga ccagctatat tccaagcggtt 300
 ttggtgtgtt cttgtcagaa gtttagtggaaa ataaacttagt gggaaatttagt ttgaaccatg 360
 agtggacatt tggaaaaactc aggccgcaca tttcacgcgg cggccaggac aaggcaggagt 420
 tgcattgtt catgctgtcg ggggtggcccg atgctgtctt tgacattcaca gacctggatg 480
 tgctaaagct tgaactaattt ccagaagcta aaattcctgc taagatttctt caaatgacta 540
 acctccaaga gctccaccc tgcactgcc ctgcggaaatgt tgaacagact gcttttagct 600
 ttcttcgcga tcacttgaga tgccttcacg tgaagttcac tggatgtggct gaaattcctg 660
 cctgggtgta ttgtctcaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720
 aaaacaataa gatgatagga cttgaatctc tccggaggtt gcccgcaccc tggatgtcc 780
 acgtgaagag caatttgacc aaagtccctt ccaacattac agatgtggctt ccacatctt 840
 caaaggtagt cattcataat gacggcacta aactcttggt actgaacagc ctttggaaaa 900
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960
 tttcagcct ctcttaattt caggaactgg attttaaagtcaataacattt cgcacaattt 1020
 agggaaatcat cagtttccag cattttaaac gactgacttg tttaaaaatta tggcataaca 1080
 aaattgttac tattccctcc tcttattaccc atgtcaaaaaa cttggagtc ctttatttctt 1140
 ctaacaacaa gotcgaatcc ttaccagtgg cagtttttttacagaaaa ctcagatgtt 1200
 tagatgttagt ctacaacaac attcaatga ttccaaataga aataggattt cttcagaacc 1260
 tgcagcattt gcatatcact ggaaacaaag tggacattctt gccaacaaat ttgtttaat 1320

gcataaaagtt gaggactttg aatctggac agaactgcat cacctcaactc ccagagaaaag 1380
 ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttgc gaccgcctgc 1440
 cagcccagct gggccagtgt cgatgctca agaaaaagccg gcttgttgta gaagatcacc 1500
 tttttgatac cctgccactc gaagtcaaag aggcatgaa tcaagacata aatattccct 1560
 ttgcaaatgg gatttaaact aagataatat atgcacagtg atgtcagga acaacttcct 1620
 agattgcaag tgctcacgta caagttatta caagataatg catttagga gtagatacat 1680
 cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
 aatgtttgta gggtttaag tcattcattt ccaaatttattt ttttttttc ttttggggaa 1800
 agggaaaggaa aaattataat cactaatctt gtttctttt aaattgtttg taacttggat 1860
 gctgccgcta ctgaatgttt acaaatttgc tgcctgctaa agtaatgtat taaattgaca 1920
 ttttcttact aaaaaaaaaa aaaaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

Met	Ala	Tyr	Met	Leu	Lys	Lys	Leu	Leu	Ile	Ser	Tyr	Ile	Ser	Ile	Ile
1				5				10					15		

Cys	Val	Tyr	Gly	Phe	Ile	Cys	Leu	Tyr	Thr	Leu	Phe	Trp	Leu	Phe	Arg
					20			25					30		

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
					35			40				45			

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
					50			55				60			

Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
					65			70			75		80		

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
					85					90			95		

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
					100			105				110			

Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
					115			120				125			

Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
					130			135				140			

Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
					145			150			155		160		

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
					165				170			175			

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
					180			185				190			

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465	470	475	480
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Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro			
485	490	495	

Phe Ala Asn Gly Ile			
500			

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 186

cctccctcta ttacccatgt c

21

<210> 187

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 187

gaccaacttt ctctggagt gagg

24

<210> 188

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 188

gtcacatttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

cccacgcgtc cggccttctc tctggacttt gcatttccat tcctttcat tgacaaactg 60
actttttta tttttttt tccatctctg ggccagctg ggatcctagg ccgccttggg 120
aagacatgg tggtttacac acataaggat ctgtgttgg ggtttcttct tcctccctg 180

acattggcat tgcttagtgg ttgtgtgggg agggagacca cgtgggctca gtgcttgctt 240
 gcacttatct gccttaggtac atcgaagtct tttgacccctc atacagtat tatgcctgtc 300
 atcgctggtg gtatcctggc ggccttgctc ctgctgatag ttgtcgtgct ctgtcttac 360
 ttcaaaatac acaacgcgct aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420
 cacaacccag acaagggtgtg gtgggccaag aacagccagg ccaaaaccat tgccacggag 480
 tcttgcctg ccctgcagtg ctgtgaagga tatagaatgt gtgcagttt tgattccctg 540
 ccacccctgct gttgcacat aaatgagggc ctctgagttt ggaaaggctc ccttctcaaa 600
 gcagagccct gaagacttca atgatgtcaa tgaggccacc tggttgtgat gtgcaggcac 660
 agaagaaaagg cacagctccc catcagttt atggaaaata actcagtgcc tgctggAAC 720
 cagctgctgg agatccctac agagagctc cactggggc aacccttcca ggaaggagtt 780
 ggggagagag aaccctact gtgggaaatg ctgataaaacc agtcacacag ctgctctatt 840
 ctcacacaaa tctacccctt gcgtggctgg aactgacgat tccctggagg tgtccagaaa 900
 gctgatgtaa cacagagccct ataaaagctg tcggtcctt aggctgcccc ggccttgcc 960
 aaaaatggagc ttgttaagaag gctcatgcca ttgaccctct taattctctc ctgtttgccg 1020
 gagctgacaa tggcgaggc tgaaggcaat gcaagctgca cagtcagttt aggggggtgcc 1080
 aatatatggcag agacccaccaa agccatgatc ctgcaactca atcccaagtga gaactgcacc 1140
 tggacaatag aaagaccaga aaacaaaagc atcagaatta tctttccctt tgccagctt 1200
 gatccagatg gaagctgtga aagtaaaaac attaaaagttt ttgacggAAC ctccagcaat 1260
 gggcctctgc tagggcaagt ctgcagttt aacgactatg ttcctgtatt tgaatcatca 1320
 tccagtagat tgcgtttca aatagttact gactcagccaa gaattcaaaag aactgtctt 1380
 gtcttctact acttcttctc tcctaaccatc tctattccaa actgtggcgg ttacctggat 1440
 accttggaaag gatccttcac cagccccaaat tacccttaccg cgcatcctga gctggcttat 1500
 tgtgtgtggc acatacaagt ggagaaaagat tacaagataa aactaaactt caaagagatt 1560
 ttcctagaaa tagacaaaaca gtgcaaattt gatttcttccatc ccatctatga tggcccttcc 1620
 accaactctg gcctgattgg acaagtcgtt ggccgtgtga ctcccacctt cgaatcgta 1680
 tcaaaactctc tgactgtcgat gttgtctaca gattatgcca atttttaccg gggattttct 1740
 gttcctaca cctcaattt tgcagaaaac atcaacacta catctttaac ttgctctct 1800
 gacaggatga gagtttattt aagcaaatttcc taccttagagg cttttaactc taatggaaat 1860
 aacttgcac taaaagaccc aacttgcaga cccaaattt caaatgttgc ggaattttct 1920
 gtcccttta atggatgtgg tacaatcaga aaggttagaaat atcagtcaat tacttacacc 1980
 aataataatca cttttcttc atcctcaact tctgaagtga tcaccgtca gaaacaactc 2040
 cagattattt tgaagtgtga aatgggacat aattctacag tggagataat atacataaca 2100
 gaagatgatg taatacaaaag tcaaaatgca ctgggcaaat ataacaccag catggcttct 2160
 tttgaatcca attcatttga aaagactata ctgaaatcacatattatgt ggatttgaac 2220
 caaactctt ttgttcaagt tagtctgcac acctcagatc caaatttggt ggtgtttctt 2280
 gatacctgtt gggcccttcc cacctctgac ttgcatttc caacctacga cctaattcaag 2340
 agtggatgtt gtcgagatgtt aacttgcataa gtgtatccct tattttggaca ctatggaga 2400
 ttccagtttta atgcctttaa atttttgcataa agttagatgtt ctgtgtatct gcagtgtaaa 2460
 gttttgatgtt gtgatagcag tgaccaccat tctcgctgca atcaaggatgtt tgtctccaga 2520
 agcaaaacgag acatttcttc atataaaatgg aaaacagatt ccatcatagg acccattcgt 2580
 ctgaaaagggtt atcgaagtgc aagtggcaat tcaggatttcc agcatgaaac acatgcggaa 2640
 gaaaactccaa accagccctt caacagtgtt catctgtttt ccttcatgtt tctagctctg 2700
 aatgtgtgtt ctgttagcgtt aatcacatgtt aggcatggatgtt taaatcaacg ggcagactac 2760
 aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtgtt gacatgtttc 2820
 tccaggatgtt caaaggaaat gctacccgtt ggctacacat attatgttataa aatgagggaaat 2880
 ggcctgaaag tgacacacacat ggcctgcattt aaaaaaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15
 Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110
 Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
 290 295 300
 Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
 325 330 335
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
 340 345 350
 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
 355 360 365
 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
 370 375 380
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
 420 425 430
 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
 435 440 445
 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
 450 455 460
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
 465 470 475 480
 Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
 500 505 510
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
 530 535 540
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
 545 550 555 560
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

565	570	575
Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe		
580	585	590
Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr		
595	600	605

<210> 191
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191
tctctattcc aaactgtggc g

21

<210> 192
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192
tttgatgacg attcgaaggt gg

22

<210> 193
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193
ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

<210> 194
<211> 2362
<212> DNA
<213> Homo sapiens

<400> 194
gacggaagaa cagcgctccc gagggccgcgg gagcctgcag agaggacagc cggcctgcgc 60
cgggacatgc ggccccagga gctccccagg ctgcgcgttcc cgttgctgtct gttgctgttgc 120
ctgctgctgc cgccgcgcgc gtgcctgcc cacagcgcca cgcgcgttcga cccccacctgg 180

gagtcctgg acgcccgcga gctgcccgcg tggtttgcacc aggcgaagtt cggcatcttc 240
 atccactggg gagtgtttc cgtgcccgac tcggtagcg agtgttctg tggtatgg 300
 caaaaaggaaa agataccgaa gtatgtggaa ttatgaaag ataattaccc tcctagttc 360
 aaatatgaag attttggacc actattaca gcaaaatttt ttaatgccaa ccagtggca 420
 gatattttc aggccctctgg tgccaaatac attgtcttaa cttccaaaca tcatgaaggg 480
 tttaccttgt ggggtcaga atattctgg aactggaatg ccatagatga ggggccccaaag 540
 agggacattg tcaaggaact tgaggtagcc attaggaaca gaactgaccc tggttttgg 600
 ctgtactatt cccttttga atggttcat ccgtcttcc ttgaggatga atccagttca 660
 ttccataagg gcacatttcc agtttctaag acattgcccag agctctatga gttagtgaac 720
 aactatcagc ctgaggttct gtggcgat ggtgacggag gaggcaccgg tcaatactgg 780
 aacagcacag gcttcttggc ctgggttat aatgaaagcc cagttcgggg cacagtagtc 840
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 gagaaggtac agtaaaaata ctgtaaaata aatggtgac cttgtataggg cacttaccac 2100
 gaatggagct tacaggactg gaagttgctc tgggtgagtc agtgggtgaa tgtgaaggcc 2160
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 ttataaaaaa aagttttctt ttcttcaatt ataaattaaac ataaatgtac tggaaacttta 2280
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 taaaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu

1

5

10

15

Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr

20

25

30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala

35

40

45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe His Trp Gly Val Phe
 50 55 60
 Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80
 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110
 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125
 Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190
 Glu Asp Glu Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220
 Leu Trp Ser Asp Gly Asp Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255
 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cggt

23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 198
 aacttgcagc atcagccact ctgc 24

<210> 199
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 199
 ttccgtgccc agcttcggta gcgagtggtt ctggtggtat tggca 45

<210> 200
 <211> 2372
 <212> DNA
 <213> Homo sapiens

<400> 200
 agcaggaaaa tccggatgtc tcggtatga agtggagcag tgagtgttag cctcaacata 60
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 catctgaggt gtttccctgg ctctgaaggg gtggcacga tggccagggtg cttcagcctg 180
 gtgttgccttc tcaactccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240
 gaagagcttt ccattccaggt gtcatgcaga attatgggta tcacccttgt gagcaaaaag 300
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 ttggccggca aggaccaagt tgaaacagcc ttgaaagctt gctttgaaac ttgcagctat 420
 ggctgggttg gagatggatt cgtggtcata tctaggatta gcccaaacc ccaagtgtggg 480
 aaaaatgggg tgggtgtctt gatggaaag gttccagtgaa gccgacagtt tgcagcctat 540
 ttttacaact catctgatac ttggactaac tcgtgcattc cagaaaattat caccacccaa 600
 gatcccatat tcaacactca aactgcaaca caaacaacag aatttttgtt cagtgcacagt 660
 acctactcg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgct 720
 ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agttttatg 780
 gaaactagca ccatgtctac agaaactgaa ccatttggta aaaataaaagc agcattcaag 840
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gactaatctt attcattttc tctaatatgg caaccattat aaccttaattt tattattaac 2220
atacctaaga agtacattgt taccttata taccaaagca cattttaaaaa gtgccattaa 2280
caaatgtatc actagccctc cttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tqtqacaaaaa aattaaagca ttttagaaaaac tt 2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
 20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
 50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
 85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
 130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 202
 gagcttcca tccaggtgtc atgc

24

<210> 203
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 203		
gtcagtgaca gtacctactc gg		22
<210> 204		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 204		
tggagcagga ggagtagtag tagg		24
<210> 205		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 205		
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt		50
<210> 206		
<211> 1620		
<212> DNA		
<213> Homo sapiens		
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<221> modified_base		
<222> (973)		
<223> a, t, c or g		
<220>		
<221> modified_base		
<222> (977)		
<223> a, t, c or g		
<220>		
<221> modified_base		
<222> (996)		
<223> a, t, c or g		
<220>		
<221> modified_base		

<222> (1003)

<223> a, t, c or g

<400> 206

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 gaaaaactgcc gccgctctgc cacggctcgc ccacccaacg cgaagacggg aaccggcttg 180
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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg

1

5

10

15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu

20

25

30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly

35

40

45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg

50

55

60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn

65

70

75

80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
290 295

<210> 208
<211> 34

<212> DNA
<213> Ant

<213> AI

三六七

<220>

<400> 208

33

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209
 tggagacaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211
 ccatttgcgtt ggaacttagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
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 gaagaagagg gcctcggggg cctccggagc tgggctttgg gcctctcctg cccacctcta 1620
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 agggggccctc aggtgtgtgt actttggaca ataaatgggt ctatgactgc cttccgc当地 1860
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<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met	Gly	Leu	Leu	Leu	Leu	Val	Pro	Leu	Leu	Leu	Pro	Gly	Ser	Tyr
1								10					15	

Gly	Leu	Pro	Phe	Tyr	Asn	Gly	Phe	Tyr	Tyr	Ser	Asn	Ser	Ala	Asn	Asp
					20			25					30		

Gln	Asn	Leu	Gly	Asn	Gly	His	Gly	Lys	Asp	Leu	Leu	Asn	Gly	Val	Lys
						35		40				45			

Leu	Val	Val	Glu	Thr	Pro	Glu	Glu	Thr	Leu	Phe	Thr	Tyr	Gln	Gly	Ala
					50			55			60				

Ser	Val	Ile	Leu	Pro	Cys	Arg	Tyr	Arg	Glu	Pro	Ala	Leu	Val	Ser
					65			70		75		80		

Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala
					85			90		95					

Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe
					100			105			110				

Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr 130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu 145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg 165	170	175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala 180	185	190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly 195	200	205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr 210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro 225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp 245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu 260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu 275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys 290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser 305	310	315
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu 325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr 340	345	350
Gly Val Tyr Cys Tyr Arg Gln His 355	360	
<210> 214		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 215

ttcccttgtg ggttggag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217

agccagttag gaaatgcg

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218

tgtccaaagt acacacacctt gagg

24

<210> 219
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 219
 gatgccacga tcgccaagggt gggacagctc tttgccgcct ggaag 45

<210> 220
 <211> 1503
 <212> DNA
 <213> Homo sapiens

<400> 220
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 tggccagggg aggggtgcacc aggccgcccc cctgagcgac gtc(cccatg atgacgccc 180
 cgggaacttc cagtacgacc atgaggctt cctgggacgg gaagtggcca aggaattcga 240
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 aaa 1503

<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
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20	25	30	
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala			
35	40	45	
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val			
50	55	60	
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu			
65	70	75	80
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp			
85	90	95	
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg			
100	105	110	
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp			
115	120	125	
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly			
130	135	140	
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr			
145	150	155	160
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp			
165	170	175	
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu			
180	185	190	
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr			
195	200	205	
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu			
210	215	220	
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala			
225	230	235	240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn			
245	250	255	
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro			
260	265	270	
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu			
275	280	285	

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt 44
 <210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens
 <400> 226
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 cacatgtatgc aggaatactt atctttcttgc ttgggtgtggc ttggggcacctt ctggatgacc 1920
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<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

Met	Ser	Ala	Ala	Trp	Ile	Pro	Ala	Leu	Gly	Leu	Gly	Val	Cys	Leu	Leu
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Leu	Leu	Pro	Gly	Pro	Ala	Gly	Ser	Glu	Gly	Ala	Ala	Pro	Ile	Ala	Ile
					20			25				30			

Thr	Cys	Phe	Thr	Arg	Gly	Leu	Asp	Ile	Arg	Lys	Glu	Lys	Ala	Asp	Val
					35			40			45				

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn
					50			55			60				

Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg
					65			70			75			80	

Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro
					85			90			95				

Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln
					100			105			110				

Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser
					115			120			125				

Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro
					130			135			140				

Thr	Gly	Lys	Arg	Leu	Lys	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys
					145			150			155			160	

Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile
					165			170			175				

Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala
					180			185			190				

Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln
					195			200			205				

Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser
					210			215			220				

Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly
					225			230			235			240	

Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe
					245			250			255				

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
 260 265 270
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
 275 280 285
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
 290 295 300
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
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 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380
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 385 390 395 400
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430
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 435 440 445
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480
 Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
 515 520 525
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228
tggtctcgca caccgatc

18

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgctgtcca caggggag

18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc

18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatagcaa ttcccgcc

18

<210> 232

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232
 ttcctcaaga gggcagcc 18

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 233
 cttggcacca atgtccgaga ttcc 24

<210> 234
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 234
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235
 <211> 2586
 <212> DNA
 <213> Homo sapiens

<400> 235
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<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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Lys	Pro	Gly	Pro	Ala	Leu	Ser	Tyr	Pro	Gln	Glu	Glu	Ala	Thr	Leu	Asn
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Leu	Arg	Ser	Ala	Val	Glu	Glu	Met	Glu	Ala	Glu	Glu	Ala	Ala	Ala	Lys
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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
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 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
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 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
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 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
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 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
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 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
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 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205

 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
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 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
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 260 265 270

 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
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 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
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 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
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<211> 3679
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<213> Homo Sapien

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<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Pro	Gln	Cys	Ala	Cys	Gln	Ile	Arg	Pro	Trp	Tyr	Thr	Pro	Arg	Ser
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Ser	Tyr	Arg	Glu	Ala	Thr	Thr	Val	Asp	Cys	Asn	Asp	Leu	Phe	Leu
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Thr	Ala	Val	Pro	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Gln	Thr	Leu	Leu
										65				75
Leu	Gln	Ser	Asn	Ser	Ile	Val	Arg	Val	Asp	Gln	Ser	Glu	Leu	Gly
					80				85					90
Tyr	Leu	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Gln	Asn	Ser	Phe
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Ser	Asp	Ala	Arg	Asp	Cys	Asp	Phe	His	Ala	Leu	Pro	Gln	Leu	Leu
					110					115				120
Ser	Leu	His	Leu	Glu	Glu	Asn	Gln	Leu	Thr	Arg	Leu	Glu	Asp	His
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Ser	Phe	Ala	Gly	Leu	Ala	Ser	Leu	Gln	Glu	Leu	Tyr	Leu	Asn	His
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 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
 185 190 195
 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
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 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu
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 230 235 240
 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
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 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
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 320 325 330
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 335 340 345
 Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
 350 355 360
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
 365 370 375
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
 380 385 390
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 395 400 405
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410	415	420
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425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
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Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
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<400> 247
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 <212> DNA
 <213> Homo Sapien

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<211> 546
<212> PRT
<213> Homo Sapien

<400> 250

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Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg	45

Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe	60

Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr	75

Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu	90

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

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Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His		
365	370	375
Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile		
380	385	390
Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu		
395	400	405
Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys		
410	415	420
Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe		
425	430	435
Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala		
440	445	450
Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln		
455	460	465
Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln		
470	475	480
Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile		
485	490	495
Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly		
500	505	510
Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp		
515	520	525
Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg		
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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

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<210> 252

<211> 24

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<400> 252
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<210> 253
<211> 47
<212> DNA
<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 253
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<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien

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tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
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gttatgtgaa tggtagtggt gcctatgccc aggacctggc tatggtggt 450
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met	Glu	Leu	Ala	Leu	Arg	Arg	Ser	Pro	Val	Pro	Arg	Trp	Leu	Leu
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Leu	Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp
														30

Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
														45
							35		40					

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
 50 55 60
 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
 65 70 75
 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
 80 85 90
 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
 95 100 105
 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
 110 115 120
 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
 125 130 135
 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
 140 145 150
 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
 155 160 165
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
 170 175 180
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
 185 190 195
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 200 205 210
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
 215 220 225
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 230 235 240
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
 245 250 255
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
 260 265 270
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
 275 280 285
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
 290 295 300
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450
 Gln Glu		
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<211> 1100		
<212> DNA		
<213> Homo Sapien		
 <400> 256		
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<210> 257
<211> 314
<212> PRT
<213> Homo Sapien
<400> 257

Met	Gly	Ala	Arg	Gly	Ala	Leu	Leu	Leu	Ala	Leu	Leu	Leu	Ala	Arg		
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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser																
														20	25	30
Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly																
														35	40	45
Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg																
														50	55	60
Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg																
														65	70	75
Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu																
														80	85	90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105

 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120

 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135

 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150

 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165

 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180

 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195

 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210

 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225

 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240

 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255

 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270

 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285

 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
 290 295 300

 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

<210> 258
 <211> 2427
 <212> DNA
 <213> Homo Sapien

<400> 258
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 cgtgcggacc ctgaggaaga gctgagtctc acctttgccccc tgagacagca 200
 gaatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250
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 <211> 556
 <212> PRT
 <213> Homo Sapien

<400> 259
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35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly
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Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser
				305					310				315	
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp
				320					325				330	
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met
				335					340				345	
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp
				350					355				360	
Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg
				365					370				375	
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly
				380					385				390	
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp
				395					400				405	
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser
				410					415				420	
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His
				425					430				435	
Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro
				440					445				450	
Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg
				455					460				465	
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val
				470					475				480	
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser
				485					490				495	
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gly
				500					505				510	
His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser
				515					520				525	
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro
				530					535				540	
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Cys

<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien

<400> 260
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tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
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 caaactttga tttttatbtc atctgaactt gtttcaaaga tttatattaa 1600
 atatttggca tacaagagat atgaaaaaaaaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Lle	Lle	Phe	Lle	Lle	Phe	Phe	Lle	Lle
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Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
														30
20														

Thr	Trp	Pro	Ala	Tyr	Arg	Lle	Pro	Val	Val	Lle	Pro	Gln	Ser	Thr
														45
35														

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
														60
50														

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
														75
65														

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Lle	Ser	Tyr	Glu	Thr	Leu
														90
80														

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
														105
95														

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
														120
110														115

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
 125 130 135
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
 140 145 150
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
 155 160 165
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
 170 175 180
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
 185 190 195
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
 200 205 210
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
 215 220 225
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 230 235 240
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 245 250 255
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
 260 265 270
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
 275 280 285
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
 290 295 300
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
 305 310 315
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
 320 325 330
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
 335 340 345
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
 350 355 360
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
 365 370 375
 Asn Tyr Leu Asp Cys Arg Glu Gly
 380

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

 <400> 262
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 caggataacct gttcccccaag cctgtggaa gccccagcag ctgaaccggg 200
 ttgtggcgg cgaggacaga actgacagcg agtggccctg gatcgtgagc 250
 atccagaaga atgggaccga ccactgcgca gggttctctgc tcaccagccg 300
 ctgggtgatc actgctgccc actgttcaa ggacaacctg aacaaaccat 350
 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
 cggtcccaga aggtgggtgt tgccctggtg gagccccacc ctgtgtattc 450
 ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctgcagcgct 500
 ccatacagtt ctcagagcgg gtcctgccc tctgcctacc tgcgttct 550
 atccacacctc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
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 aataggctca tctacctcta cctctggggg cccggacggc tgctgcggaa 1150

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 ataaattatt tattctccaa aaaaaaaaa 1378
 <210> 263
 <211> 317
 <212> PRT
 <213> Homo Sapien
 <400> 263

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				20					25					30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35					40					45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50				55						60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65				70						75
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80					85					90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95					100					105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110					115					120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125					130					135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140					145					150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155					160					165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
				170					175					180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
 185 195
 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
 200 205 210
 Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
 215 220 225
 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 230 235 240
 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
 245 250 255
 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
 260 265 270
 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
 275 280 285
 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
 290 295 300
 Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
 305 310 315

Arg Ser

<210> 264
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 264
gtccgcaagg atgcctacat gttc 24

<210> 265
<211> 19
<212> DNA
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<220>
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<400> 265
gcagaggtgt ctaaggttg 19

<210> 266
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
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<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
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<400> 267
gccaccaact cctgcaagaa ctttcagaa ctgcccctgg tcattg 45

<210> 268
<211> 25
<212> DNA
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<220>
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<400> 268
ggggaaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
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<220>
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<400> 271
gcggaagggc agaatggac tccaaag 26

<210> 272
<211> 18
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

<212> DNA
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<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccgaggc ccgac 45

<210> 276
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<220>
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<400> 276
ggcagggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280
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<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gctccataca gttcccttgc cccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282
tggaggggga gcgggatgct tgtctggcg actccggggg cccccctcatg 50

tgcagggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283
ccctcagacc ctgcagaaggc tgaagggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcg ggagcaggac agggaccat cactgaggac 100

atgtctgttg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggc ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgttga tggtgagat gcacaacctc tacccggccc 150
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
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 caaggagcgc gggcgccgag gcgagaatct gttcgccatc acagacgagg 300
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 gttcctatcc caaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000
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<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu
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Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
									20					30

Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
									35					45

Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
								50						60

Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
								65						75

Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe
								80						90

Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
									95					105

Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
								110						120

Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
									125					135

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
 455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

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<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 288

atgaggagaa acgtttgatg gtggagctgc acaacacctcta ccggg 45

<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaaactga 200
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tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150
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actacaggac tccaaatttt cagtcttatg acttggacac atagactgaa 3250
tgagaccaaa ggaaaagctt aacatactac ctcaagtgaa cttttattta 3300
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ataaaaaatgc ttatattata cagatgaacc aaaattacaa aaagtttatg 3400
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tttttaact ttgttttatg caaaaaagta tcttacgtaa attaatgata 3500
taaatcatga ttattttatg tattttata atgccagatt tcttttatg 3550
gaaaatgagt tactaaagca ttttaataa tacctgcctt gtaccatttt 3600
ttaaatagaa gttacttcat tatatttgc acattatatt taataaaaatg 3650
tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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1 5 10

15

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Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
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 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
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 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
 65 70 75
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
 80 85 90
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
 95 100 105
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
 110 115 120
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
 125 130 135
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
 140 145 150
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
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 Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
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 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
 185 190 195
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
 200 205 210
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
 215 220 225
 Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
 230 235 240
 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
 245 250 255
 Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
 260 265 270
 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
 275 280 285
 Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

290	295	300
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
305	310	315
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
455	460	465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
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 Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
 575 580 585

 Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
 590 595 600

 Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
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 Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
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 Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
 635 640 645

 Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
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 Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
 665 670 675

 Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
 680 685 690

 Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
 695 700 705

 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
 710 715 720

 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 725 730 735

 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 740 745 750

 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 755 760 765

 Trp Val Val Ile Ile Tyr His Thr Arg Arg Asn Glu Asp Cys
 770 775 780

 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 785 790 795

 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 800 805 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
 950 955 960
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
 980 985 990
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
 1010 1015 1020
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
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 <211> 2906

<212> DNA
<213> Homo Sapien

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met	Leu	Asn	Lys	Met	Thr	Leu	His	Pro	Gln	Gln	Ile	Met	Ile	Gly
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						20				25				30
Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln
						35			40					45
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val
											55			60
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser
						65			70					75
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile
						80			85					90
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu
						95			100					105
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe
						110			115					120
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg
						125			130					135
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu
						140			145					150
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser

155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly		
170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys		
320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp		
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys		
365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val		
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
 425 430 435
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
 440 445 450
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
 455 460 465
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
 470 475 480
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
 485 490 495
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
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 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
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 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
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 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
 545 550 555
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
 560 565 570
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
 575 580 585
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
 590 595 600
 Tyr Lys Ser Pro Phe Asn His Thr Thr Val Asn Thr Ile Asn
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<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met	Ser	Ala	Pro	Ser	Leu	Arg	Ala	Arg	Ala	Ala	Gly	Leu	Gly	Leu
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Leu	Leu	Cys	Ala	Val	Leu	Gly	Arg	Ala	Gly	Arg	Ser	Asp	Ser	Gly
					20				25				30	

Gly	Arg	Gly	Glu	Ieu	Gly	Gln	Pro	Ser	Gly	Val	Ala	Ala	Glu	Arg
					35				40				45	

Pro	Cys	Pro	Thr	Thr	Cys	Arg	Cys	Ieu	Gly	Asp	Leu	Leu	Asp	Cys
					50				55				60	

Ser	Arg	Lys	Arg	Ieu	Ala	Arg	Ieu	Pro	Glu	Pro	Leu	Pro	Ser	Trp
					65				70				75	

Val	Ala	Arg	Ieu	Asp	Ieu	Ser	His	Asn	Arg	Ieu	Ser	Phe	Ile	Lys
					80				85				90	

Ala	Ser	Ser	Met	Ser	His	Ieu	Gln	Ser	Ieu	Arg	Glu	Val	Lys	Ieu
					95				100				105	

Asn	Asn	Asn	Glu	Ieu	Glu	Thr	Ile	Pro	Asn	Ieu	Gly	Pro	Val	Ser
					110				115				120	

Ala	Asn	Ile	Thr	Ieu	Ieu	Ser	Ieu	Ala	Gly	Asn	Arg	Ile	Val	Glu
					125				130				135	

Ile	Ieu	Pro	Glu	His	Ieu	Lys	Glu	Phe	Gln	Ser	Ieu	Glu	Thr	Ieu
					140				145				150	

Asp	Ieu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Ieu	Gln	Thr	Ala	Phe	Pro
					155				160				165	

Ala	Ieu	Gln	Ieu	Lys	Tyr	Ieu	Tyr	Ieu	Asn	Ser	Asn	Arg	Val	Thr
					170				175				180	

Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Ieu	Ala	Asn	Thr	Ieu	Ieu
					185				190				195	

Val	Ieu	Lys	Ieu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
					200				205				210	

Met Phe Lys Ieu Pro Gln Ieu Gln His Ieu Glu Ieu Asn Arg Asn

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Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala		
230	235	240
Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		
245	250	255
Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu		
260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
440	445	450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
455	460	465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
485	490	495
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
500	505	510
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
515	520	525
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
530	535	540
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
545	550	555
Gly Gly Glu Val Met Glu Tyr Thr Ile Leu Arg Leu Arg Glu		
560	565	570
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
575	580	585
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
590	595	600
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
605	610	615
Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro		
620	625	630
Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro		
635	640	645
Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val		
650	655	660
Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser		
665	670	675
Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr		
680	685	690
Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp		
695	700	705
Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala		
710	715	720
Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser		
725	730	735
Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln		
740	745	750

Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
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 Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
 770 775 780
 Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
 785 790 795
 Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
 800 805 810
 Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 815 820 825
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
 830 835 840
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 845 850 855
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 860 865 870
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 875 880 885
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 890 895 900
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
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 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 920 925 930
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 935 940 945
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 950 955 960
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 965 970 975
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 980 985 990
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 995 1000 1005
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu

1010 1015 1020
Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
1025 1030 1035
Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
1040 1045 1050
Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
1055 1060 1065
Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1070 1075 1080
Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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Asn Phe Gln Ser Tyr Asp Leu Asp Thr
1115

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<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 295
ggaaccgaat ctcagcta 18

<210> 296
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 296
cctaaaactga actggacca 19

<210> 297
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 297
ggctggagac actgaacct 19

<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 298
acagctgcac agtcagaac agtg 24

<210> 299

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 299
cattcccagt ataaaaatcc tc 22

<210> 300
<211> 18
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 300
gggtcttgggt gaatgagg 18

<210> 301
<211> 24
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 301
gtgcctctcg gttaccacca atgg 24

<210> 302
<211> 50
<212> DNA
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<220>
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<400> 302
gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303
<211> 28
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 303
gccttgaca accttcagtc actagtgg 28

<210> 304
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 304
ccccatgtgt ccatgactgt tccc 24

<210> 305
<211> 45
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 305
tactgcctca tgacctttc actcccttgc atcatcttag agcgg 45

<210> 306
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 306
actccaaggaa aatcggttcc gttc 24

<210> 307
<211> 24

<212> DNA
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 307
 ttagcagctg aggatggca caac 24

<210> 308
 <211> 24
 <212> DNA
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 <220>
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 <400> 308
 actccaagga aatcggttcc gttc 24

<210> 309
 <211> 50
 <212> DNA
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 <400> 309
 gcatttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310
 <211> 3296
 <212> DNA
 <213> Homo Sapien

<400> 310

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 gcgcccgctcg gcgccggggc gcagcaggaa agggaaagct gtggtctgcc 150
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 ccgtcccccta tccctccctt atatagaaac cttccacact gggaaaggcag 250
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<210> 311
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 311
gcattggccg cgagactttg cc 22

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 312
gcggccacgg tccttgaaaa tg 22

<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 313
tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien

<400> 314
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cgccgctgtc ctccgggagc ggcagcagta gccccggcgg cgagggctgg 100

gggttcctcg agactctcag aggggcgcct cccatcgccg cccaccaccc 150
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catcttgttt attatttaat gtttctaaa ataaaaaaatg ttagtggttt 2950
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aat 3003

<210> 315
<211> 509
<212> PRT
<213> Homo Sapien

<400> 315
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Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val
20 25 30
Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys
35 40 45
Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
50 55 60
Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
65 70 75
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
80 85 90
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
95 100 105
Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
110 115 120
Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
125 130 135
Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
140 145 150
Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
155 160 165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170 175 180
 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185 190 195
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200 205 210
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215 220 225
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230 235 240
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245 250 255
 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
 260 265 270
 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
 275 280 285
 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
 290 295 300
 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
 305 310 315
 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
 320 325 330
 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
 335 340 345
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
 350 355 360
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
 365 370 375
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
 380 385 390
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
 395 400 405
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
 410 415 420
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425	430	435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly		
440	445	450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser		
455	460	465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala		
470	475	480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln		
485	490	495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg		
500	505	

<210> 316
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 316
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<210> 317
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 317
ttgcacttgtt aggacccacg tacg 24

<210> 318
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 318
ctgatggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319
<211> 2110
<212> DNA

<213> Homo Sapien

<400> 319

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 atcactatcc ttgatttatcc ccatgtgtct tctcttccta tggaaaaaat 1150
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aaaaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met	Trp	Leu	Lys	Val	Phe	Thr	Thr	Phe	Leu	Ser	Phe	Ala	Thr	Gly
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Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
20 25 30

Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
35 40 45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
50 55 60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225
 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
 230 235 240
 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
 245 250 255
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
 260 265 270
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
 275 280 285
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
 290 295 300
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
 305 310 315
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
440	445	450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatccctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 323
ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

<210> 324
<211> 2397
<212> DNA
<213> Homo Sapien

<400> 324
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acgttcgctg catcacggac gagaactgga gagaactgct ggaaggagac 150
tggatgatag aattttatgc cccgtggtgc cctgcttgc aaaatctca 200
accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250
ttgcgaaaatg agatgtcaca gagcagccag gactgagtgg acggtttatac 300
ataactgctc ttcctactat ttatcattgt aaagatggtg aatttaggcg 350
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aagagtggaa gagtatttag cccgtttcat catggttgg tccaggttct 450
gttctgatga gtagtatgtc agactcttt cagctatcta tgtggatcag 500
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550
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aaccttgaa aaaagtggag gaggaacaag aggccgatga agaagatgtt 750
tcagaagaag aagctgaaag taaaagaagga acaaacaag actttccaca 800
gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900
aagattgatc attttgtttg gtttgaagtg aactgtgact tttttgaata 950
ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

acataaaaagc actaggata caagtttcaa atatgattt agcacagtat 1050
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atttatgtat atttggtttaa taataaccta tttcaagtct gagttttcaa 1150
aatttacatt tcccaagttat tgcattattt aggtatttaa gaagatttatt 1200
ttagagaaaa atatttctca tttgatataa tttttctctg tttcaactgtg 1250
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caaattggat gataatttct tgaaacatt ttttatgttt tagtaaacag 1600
tatttttttgc ttgtttcaaa ctgaagtttca ctgagagatc catcaaatttgc 1650
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cattcttgcgt gaacttcaac ttgaaattgt ttttttttgc tttttggatg 1750
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aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaaa 2397

<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

Met	Ala	Pro	Ser	Gly	Ser	Leu	Ala	Val	Pro	Leu	Ala	Val	Leu	Val
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						5				10				15

Leu	Leu	Leu	Trp	Gly	Ala	Pro	Trp	Thr	His	Gly	Arg	Arg	Ser	Asn
						20				25				30

Val	Arg	Val	Ile	Thr	Asp	Glu	Asn	Trp	Arg	Glu	Leu	Leu	Glu	Gly
						35			40					45

Asp	Trp	Met	Ile	Glu	Phe	Tyr	Ala	Pro	Trp	Cys	Pro	Ala	Cys	Gln
						50			55					60

Asn	Leu	Gln	Pro	Glu	Trp	Glu	Ser	Phe	Ala	Glu	Trp	Gly	Glu	Asp
						65			70					75

Leu	Glu	Val	Asn	Ile	Ala	Lys	Val	Asp	Val	Thr	Glu	Gln	Pro	Gly
						80			85					90

Leu	Ser	Gly	Arg	Phe	Ile	Ile	Thr	Ala	Leu	Pro	Thr	Ile	Tyr	His
						95			100					105

Cys	Lys	Asp	Gly	Glu	Phe	Arg	Arg	Tyr	Gln	Gly	Pro	Arg	Thr	Lys
						110			115					120

Lys	Asp	Phe	Ile	Asn	Phe	Ile	Ser	Asp	Lys	Glu	Trp	Lys	Ser	Ile
						125			130					135

Glu	Pro	Val	Ser	Ser	Trp	Phe	Gly	Pro	Gly	Ser	Val	Leu	Met	Ser
						140			145					150

Ser	Met	Ser	Ala	Leu	Phe	Gln	Leu	Ser	Met	Trp	Ile	Arg	Thr	Cys
						155			160					165

His	Asn	Tyr	Phe	Ile	Glu	Asp	Leu	Gly	Leu	Pro	Val	Trp	Gly	Ser
						170			175					180

Tyr	Thr	Val	Phe	Ala	Leu	Ala	Thr	Leu	Phe	Ser	Gly	Leu	Leu	Leu
						185			190					195

Gly	Leu	Cys	Met	Ile	Phe	Val	Ala	Asp	Cys	Leu	Cys	Pro	Ser	Lys
						200			205					210

Arg	Arg	Arg	Pro	Gln	Pro	Tyr	Pro	Tyr	Pro	Ser	Lys	Lys	Leu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

215 220 225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240
Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu
245 250 255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280

<210> 326
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 326
tgaggtgggc aagcggcgaa atg 23

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 327
tatgtggatc aggacgtgcc 20

<210> 328
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
tgcagggttc agtcttagatt g 21

<210> 329
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
gcgagtgtcc agctgcggag acccgtgata attcgtaac taattcaaca 50
aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100
ggacaggcgg attggaagag cggaaaggtc ctggccaga gcagtgtgac 150
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300
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gaaggggact attatcatac ggtgttgtgg atggagcagg tgctaaagca 750

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gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val
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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
				20					25				30	

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35				40					45	

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50				55				60		

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65				70				75		

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80				85				90		

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95					100				105	

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110				115					120	

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125				130				135		

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140				145				150		

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155				160				165		

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170				175				180		

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185				190				195		

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu	
				200				205				210		

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg
 215 220 225
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
 230 235 240
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu
 245 250 255
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu
 260 265 270
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
 275 280 285
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
 290 295 300
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
 305 310 315
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
 320 325 330
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
 335 340 345
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
 350 355 360
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
 365 370 375
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp
 380 385 390
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
 395 400 405
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
 410 415 420
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
 425 430 435
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
 440 445 450
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr
 455 460 465
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
 470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccagggcacaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 335

ggtctcaaga actcctgtc 19

<210> 336

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
ggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

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 cccgtgggc tccctgctcc tttcacacca cactctcgct ttgaggtgct 1450
 gggctggac tacttcacag agcagcacac cttctctgt gcagatgggg 1500
 ctcccaagtg cccactacag ggggctagca gggcggacgt gggtgatgcg 1550
 ttggagactg ccctggagca gctcaatcgg cgctatcage cccgcctgctg 1600
 cttccagaag cagcgactgc tcaacggcta tcggcgcttc gacccagcac 1650
 gggcatgga gtacaccctg gacctgtgt tggaatgtgt gacacagcgt 1700
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 agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggcttcc 1850
 ctcgaggcgt ttgcagccaa tgcctggag ccacgagaac atgcattgct 1900
 cacccctgttg ctggtctacg ggcacgaga aggtggccgt ggagctccag 1950
 acccattttct tgggggtgaag gctgcagcag cggagttaga ggcacggta 2000
 cctgggacga ggctggcctg gctcgctgtg cgagcagagg ccccttccca 2050
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tgtcgcatga atgccatctc tggctggcag gccttcttc cagtcattt 2200
ccaggagttc aatcctgccc tgtcaccaca gagatcaccc ccagggcccc 2250
cgggggctgg ccctgacccc ccctccctc ctggtgctga cccctccgg 2300
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gttttctcc gtttctcagg gctccacctc ttccggcccg tagagccagg 2500
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ggccgcctgg gggccctaac ctcattacct ttcccttgc tgcctcagcc 2700
ccaggaaggg caaggcaaga tggtgacag atagagaatt gttgctgtat 2750
tttttaataaata taaaaatgtt attaaacatq ttttctqcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro
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Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg
20 25 30

Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala
35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val	
110	115	120
Asn Arg Thr Val Ala His His Phe Pro	Arg Leu Leu Tyr Phe Thr	
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala	Gly Met Gln Val Val Ser	
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu	Met Ser Glu Thr Leu Arg	
155	160	165
His Leu His Thr His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile	
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala	Pro Arg Leu Ala Ala Leu	
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala	
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln	Ala Arg Tyr Cys His Gly	
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg	
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro	
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile	Asp Ser Leu Gly Val Gly	
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu	
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu	Gly Ser Ser Ala Phe Leu	
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr	
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu	Glu Leu Glu Arg Ala Tyr	
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val	
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu	Ser Trp Pro Val Gly Leu	
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
 365 370 375
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
 380 385 390
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
 395 400 405
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
 410 415 420
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
 425 430 435
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
 440 445 450
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
 455 460 465
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
 470 475 480
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
 485 490 495
 Leu Val Ala Glu Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
 500 505 510
 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
 515 520 525
 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
 530 535 540
 Pro Phe Leu Gly Val Lys Ala Ala Ala Glu Leu Glu Arg Arg
 545 550 555
 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
 560 565 570
 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
 575 580 585
 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
 590 595 600
 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
 605 610 615
 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
 755 760 765
 Gln Glu Gln Ala Asn Ser Thr
 770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340
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 tgcgttcaag ccgttctaga cgcggaaaa atgctttctg aaagcagctc 100
 cttttgaag ggtgtatgc ttggaagcat ttctgtgct ttgatcacta 150
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
 catcatcacc tacaagctcc taacaaagaa gatatctga aaatttcaga 250
 ggatgagcgc atggagctca gtaagagctt tcgagttatac tgtattatcc 300
 ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350
 accaaacact gtgacaaaagc agagttcttc agttctgaaa atgttaaagt 400

gttttagtca attaatatgg acacaaatga catgtggta atgatgagaa 450
 aagcttacaa atacgcctt gataagtata gagaccaata caactggtc 500
 ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt 550
 tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750
 cagtttgcct gaaatatgct ggagtattt cagaaaatgc agaagatgct 800
 gatggaaaag atgtatttaa taccaaatac gttgggcttt ctattaaaga 850
 ggcaatgact tatcacccca accaggtgt agaaggctgt tggtcagata 900
 tggctgttac tttaatggc ctgactccaa atcagatgca tgtgtatgt 950
 tatgggttat accgccttag ggcatttggg catatttca atgatgcatt 1000
 ggtttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050
 agcgtgaata tgatcttgt ataggacgtg tggtgtcatt attttagt 1100
 gtaactacat atccaataaca gctgtatgtt tcttttctt ttctaattt 1150
 gtggcactgg tataaccaca cattaaagtc agtagtacat tttaaatga 1200
 gggtggtttt ttctttaaa acacatgaac attgtaaatg tggtggaaag 1250
 aagtgtttta agaataataa tttgcaaataa aaactattaa taaatattat 1300
 atgtgataaa ttcttaattt tgaacattttt aaatctgtgg ggcacatattt 1350
 tttgctgatt ggttaaaaaa tttaacagg tctttagcgt tctaagat 1400
 gcaaataatgata tctctagttt tgaatttgcgt attaaagtaa aacttttagc 1450
 tgggtgttcc cttaatctt aatactgatt tatgttctaa gctccccaa 1500
 gttccaaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550
 attaaagtga aagttgaaaaa at 1572

<210> 341
 <211> 318
 <212> PRT
 <213> Homo Sapien

<400> 341
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 Ser Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile
 20 25 30
 Gly His Gly Asn Arg Met His His His His His His His Leu Gln
 35 40 45
 Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg
 50 55 60
 Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val
 65 70 75
 Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp
 80 85 90
 Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val
 95 100 105
 Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu
 110 115 120
 Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp
 125 130 135
 Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile
 140 145 150
 Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln
 155 160 165
 Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr
 170 175 180
 Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys
 185 190 195
 Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln
 200 205 210
 Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val
 215 220 225
 Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
 230 235 240
 Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile
 245 250 255
 Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys

260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
290 295 300

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345
gggtgtatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346
gggatgcagg tggtgtctca tgggg 25

<210> 347
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347
ccctcatgta ccggctcc 18

<210> 348
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348
ggattctaat acgactcact atagggtca gaaaagcgca acagagaa 48

<210> 349
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349
ctatgaaatt aaccctcact aaaggatgt cttccatgcc aaccttc 47

<210> 350
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 350
ggattctaat acgactcaact atagggcggc gatgtccact ggggctac 48

<210> 351
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 351
ctatgaaatt aaccctcaact aaagggacga ggaagatggg cggatgg 48

<210> 352
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 352
ggattctaat acgactcaact atagggcacc cacgcgtccg gctgatt 47

<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 353
ctatgaaatt aaccctcaact aaagggacgg gggacaccac ggaccaga 48

<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 354
ggattctaat acgactcaact atagggcttg ctgcggttt tgttcctg 48

<210> 355
<211> 48

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 355
ctatgaaatt aaccctcact aaagggagct gccgatccca ctggatt 48

<210> 356
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 356
ggattctaat acgactcact atagggcgga tcctggccgg cctctg 46

<210> 357
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 357
ctatgaaatt aaccctcact aaagggagcc cggcatggt ctcagtta 48

<210> 358
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 358
ggattctaat acgactcact atagggcgga aagatggcga ggaggag 47

<210> 359
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 359
ctatgaaatt aaccctcact aaagggacca aggccacaaa cggaaatc 48

<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 360
ggattctaat acgactcact atagggctgt gctttcattc tgccagta 48

<210> 361
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 361
ctatgaaatt aaccctcact aaaggaggg tacaattaag gggtggat 48

<210> 362
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 362
ggattctaat acgactcact atagggcccg cctcgctcct gotcctg 47

<210> 363
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 363
ctatgaaatt aaccctcact aaaggaggga ttgccgcgac cctcacag 48

<210> 364
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 364

ggattctaat acgactcact atagggcccc tcctgccttc cctgtcc 47
<210> 365
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 365
ctatgaaatt aaccctcact aaaggagtg gtggccgcga ttatctgc 48

<210> 366
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 366
ggattctaat acgactcact atagggcgca gcgatggcag cgatgagg 48

<210> 367
<211> 47

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 367
ctatgaaatt aaccctcact aaaggacag acggggcaga gggagtg 47

<210> 368
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 368
ggattctaat acgactcact atagggccag gaggcgtgag gagaaac 47

<210> 369
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369
ctatgaaatt aaccctcact aaaggaaag acatgtcata gggagtgg 48

<210> 370
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 370
ggattctaat acgactcact atagggccgg gtggagggtgg aacagaaaa 48

<210> 371
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 371
ctatgaaatt aaccctcact aaaggacac agacagagcc ccatacgc 48

<210> 372
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 372
ggattctaat acgactcact atagggccag ggaaatccgg atgtctc 47

<210> 373
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 373
ctatgaaatt aaccctcact aaaggagta agggatgcc accgagta 48

<210> 374
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 374

ggattctaat acgactcaact atagggccag ctacccgcag gaggagg 47

<210> 375

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

ctatgaatt aaccctcaact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaaagag 50

agggagggag agaaaaaagag agagagagaa acaaaaaacc aaagagagag 100

aaaaaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150

tgcttcctttt cccaaatgtt cttatggact gttgctggta tccccatcct 200

atttctcaatgtt gcctgtttca tcaccagatg tggtgtgaca tttcgcatct 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

cttcctgtt acaattatgg atcaggttca gtcaagaatt gttgtccatt 350

gaactggaa tattttcaat ccagctgcta cttctttct actgacacca 400

tttcctgggc gttaagtta aagaactgct cagccatggg gggtcacctg 450

gtggttatca actcacagga ggagcaggaa ttcccttcct acaagaaaacc 500

taaaaatgaga gagttttta ttggactgtc agaccagggtt gtcgagggtc 550

agtggcaatg ggtggacggc acaccttga caaagtctct gagcttctgg 600

gatgttagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650

gagagactct tcaaacccaa ggcaaaattg gaatgatgta acctgtttcc 700

tcaatttattt tcggatttgt gaaatggtag gaataaatcc tttgaacaaa 750

ggaaaatctc tttttaagaaca gaaggcacaa ctc当地atgtg taaaagaagga 800
 agagcaagaa catggccaca cccaccgccc cacacgagaa atttgtgcgc 850
 tgaacttcaa aggacttcat aagtatttgt tactctgata caaataaaaa 900
 taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377

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Cys	Phe	Ser	Ser	Gln	Met	Phe	Leu	Trp	Thr	Val	Ala	Gly	Ile	Pro
				20				25					30	
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
				35				40					45	
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
				50				55					60	
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser
				65				70					75	
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
				80				85					90	
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
				95				100					105	
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
				110				115					120	
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
				125				130					135	
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
				140				145					150	
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
				155				160					165	
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
				170				175					180	

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
215

<210> 378
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 378
ttcagcttct gggatgtagg g 21

<210> 379
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 379
tattcctacc atttcacaaa tccg 24

<210> 380
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 380
ggaggactgt gccaccatga gagactttc aaacccaagg caaaattgg 49

<210> 381
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
gcagatttg aggacagcca cctcca 26

<210> 382
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
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Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310